

## STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 190167

TO: Manjunath N Rao

Location: rem/2A01/2C70

Art Unit: 1652

Friday, May 19, 2006

Case Serial Number: 09/211691

From: Barb O'Bryen

**Location: Biotech-Chem Library** 

Remsen 1a69

Phone: 571-272-2518

- B

barbara.obryen@uspto.gov

Search Notes		And the second s
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#### STIC-Biotech/ChemLib

190167

My

From:

Chan, Christina

Sent:

Tuesday, May 16, 2006 1:53 PM

To:

Rao, Manjunath N.; STIC-Biotech/ChemLib

Subject:

RE: RUSH sequence search request for 09/211691

Please rush! Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841

Remsen, 3E89

CECEIVED

----Original Message-----

From:

Rao, Manjunath N.

Sent:

Tuesday, May 16, 2006 1:50 PM

To:

Chan, Christina

Subject:

RUSH sequence search request for 09/211691

Hello Christina,

Please authorize the request below as RUSH. The reason being, this is an RCE and applicants have now included the following sequences in their claims.

Many Thanks -Manjunath

Manjunath N. Rao
Art Unit 1652, Room 2A01,
Mail Box in Room 2C70,
Remsen Building, USPTO
400, Dulany St.
Alexandria, VA.
Phone: 571-272-0939

From: Manjunath N. Rao

Art Unit 1652, Room 2A01 Mail Box in Room 2C70

Phone: 272-0939

Date: 5-16-06

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type (	of Search
NA#	_ AA#:
S/L: O	ligomer:
Encode/Trans	sl:
Structure #:_	Text:
Inventor:	Litigation:

*********
Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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Please search the following as soon as possible for application with serial number **09/211691** 

1. SEQ ID NO: 5 and 6 against all <u>commercial nucleic acid sequence databases</u>, <u>issued</u>

<u>patents/published applications nucleic acid sequence database</u> and <u>pending</u>

<u>application nucleic acid sequence database</u>. Please provide a <u>print</u> of <u>results</u>

If you have any questions please call me at the above phone number.

**Thanks** 

Searcher: \_\_\_\_\_\_
Searcher Phone: \_\_\_\_\_\_
Date Searcher Picked up: \_\_\_\_\_
Date completed: \_\_\_\_\_
Searcher Prep Time: \_\_\_\_\_
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T	ype of Search
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Inventor	Litigation:

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SUMMARIES
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Result	Score	Query Match	Query Match Length DB	DB	ID	Description
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2	26.4	71.4	110000	15	AE002098 09	Continuation (10 o
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œ	26	70.3	1116	N	AR105309	AR105309 Sequence
9	26	70.3	1116	N	AR144756	AR144756 Sequence
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11	26	70.3	1116	15	NMU60661	U60661 Neisseria m
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### ALIGNMENTS

CDS	FEATURES source	JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 NMU60660 LOCUS DEFINITION
/ Organis   No. 1   No.   No.	UKO, Cataga Location/Qualifiers 12039	gonorrhoeae J. Biol. Chem. 271 (45), 28271-28276 (1996) 8910446 2 (bases 1 to 2039) 2 (bases n. Michniewicz, J.J., Watson, D.C. and Wakarchuk, W.W. Direct Submission Submitted (13-JUN-1996) Institute for Biological Sciences, National Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario KIA	Neisseriaceae; Neisseria.  Neisseriaceae; Neisseria.  1 (bases 1 to 2039)  Gilbert,M., Watson,D.C., Cunningham,A.M., Jennings,M.P., Young,N.M. and Wakarchuk,W.W.  Cloning of the lipooligosaccharide alpha-2,3-sialyltransferase from the bacterial pathogens Neisseria meningitidis and Neisseria		NMU60660 2039 bp DNA linear BCT 08-NOV-1996 Neisseria meningitidis alpha-2,3-sialyltransferase gene, complete cds, and isocitrate dehydrogenase and cytochrome c genes, partial

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RESULT 2
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WPCOMMENT
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/transl_table=11
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; Neisseria

1 (bases 1 to 331801)

12 Parkhill, J., Achtman, M., James, K.D., Bentley, S.D., Churcher, C., Klee, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T., Davies, R.M., Davis, P., Devlin, K., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Moule, S., Mungall, K., Quail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Quail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Skelton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G. Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491

Nature 404 (6777), 502-506 (2000)
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Neisseria meningitidis Z2491
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/gene="NNA1040"
/gene="NNA1040, possible type I restriction-modification
/note="NNA1040, possible type I restriction-modification
system specificity protein, pseudogene, len: 1217 bp;
N-terminus shows weak similarity to the C-terminal half of
TR:050359 (EMBL:L25415), hsdS1B, Mycoplasma pulmonis
restriction-modification enzyme subunit S1B (336 aa),
fasta scores; E(): 2.3e-06, 26.2% identity in 141 aa
overlap and to many hypothetical restriction-modification
subunits. Also similar to NNA1041, fasta scores; E():
4.8e-10, 37.0% identity in 100 aa overlap. C-terminus
similar to part of SW:TIS1_ECOLI (EMBL:XI3145), hsdS,
Escherichia coli type I restriction enzyme EcoR124II
specificity protein (410 aa), fasta scores; E(): 1.9e-14,
39.6% identity in 182 aa overlap. Similar to NNA1040, E():
2.9e-09, 38.0% identity in 100 aa overlap. Contains Pfam
match to entry PF01420 Methylase S, Type I restriction
modification DNA specificity domain. Contains a G(8) tract
which would allow translation as an intact CDS, if
variable. Lies within a region of unusually low GC
                                 /pseudo
/codon_start=1
/transl_table=1
   /transl_table=11
/product≃"pseudogene
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/note="serogroup: A"
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/mol_type="genomic DNA"
/strain="Z2491"
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complement (4559. .6838)

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/note="Pfam match to entry PF01420 Methylase_S, Type I
restriction modification DNA specificity domain, score
105.50, E-value 1.1e-27"
                                                                                                           complement (4531. .4540)
/note="Core DNA uptake sequence:
                                                                                                                                                                                                                                                                   4514. 4945
/note="Stem loop containing DNA uptake sequences:
gcogtotgaa at ttcagacggc atttt"
4519. 4528
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complement(1642. .1651)
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/note="Core DNA uptake sequence: gccgtctgaa"
                                       complement (4559. .6838)
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/gene="NMA1042"
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/transl_table=11
/product="type I restriction-modification system/product="type I restriction-modification" system/product="type I restriction-modification-modification" system/product="type I restriction-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modification-modifica
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1415. .4509
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/gene="NMA1042"
                                                                               /label=DUS
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                                                                                                                                                                                                                                                                                                                                                         /gene="NMA1046"
complement (6842. .7153)
/gene="NMA1046"
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complement(5330. .5353)
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complement (5894. .5932)
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/transl_table=11
/product="putative ATP-dependent protease ATP-binding
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/db_xref="GOA:Q9JV15"
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Neisseria meningitidis
Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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CHIRON '
                                                                                                                                                                                                                                                                                Pizza, M.
                                                                                                                                                                                                                                                                                                                                                                        CS238430.1 GI:84364857
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Neisseria meningitidis
Bacteria; Protectia; Betaproteobacteria; Neisseriales;
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        Conservative
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                                                                /note="seq 1 to long, 2242716 replaced by new seq 1, from 1 to 34 seq 110, from 300001 to 649980 seq 111, from 600001 to 1249980 seq 112, from 900001 to 1249980 seq 113, from 1200001 to 1549980 seq 114, from 1500001 to 1549980 seq 115, from 1800001 to 2149980 seq 116, from 1800001 to 2242716"
                                                                                                                                                                                                                                   : EP 1605061-A 112 14-DEC-2005;
CORPORATION (US); THE INSTITUTE
Location/Qualifiers
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CORPORATION (US); THE INSTITUTE
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                                                                                                                                                                                                                                                                                                                                                                                                 112 from
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/mol_type="unassigned DNA"
/db_xref="taxon:487"
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/db_xref="taxon:487"
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|mol_type="unassigned DNA"
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                 71.48;
96.48;
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96.48;
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  Score 26.4; DB Pred. No. 0.78; Mismatches
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Pizza,M., Hickey,E., Peterson,J., Tettelin,H., Venter,J.C., Masignani,V., Galeotti,C., Mora,M., Ratti,G., Scarselli,M., Scarlato,V., Rappuoll,R., Frazer,C.M. and Grandi,G. Neisseria genomic sequences and methods of their use Patent: WO 0066791-A 110 09-NOV-2000; CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCY LOCALION/Qualifiers
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Neisseria meningitidis
Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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AX044031
AX044031.1 GI:11342915
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27; Conserv
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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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llarity 96.4%;
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/mol_type="unassigned DNA"
/db_xref="taxon:487"
/note="sequence too long, cut in 8
seq 1: 1 to 349980 349980 bases
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/mol_type="unassigned DNA"
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Sequence 1 from patent US 6096529.
AR105309
                                                                                                               Recombinant .alpha.-2,3-sialyltransferases
Patent: US 6210933-A 1 03-APR-2001;
Location/Qualifiers
                                                                                                                                                              1 (bases 1 to 1116)
Gilbert, M., Wakarchuk, W.W., Young, N.Martin., Jennings, M.P.
                                                                                                                                                                                                       Unknown
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                                                                                                                                                      Moxon, E. Richard
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109: 600001 to 949980 349980 bases
110: 900001 to 1249980 349980 bases
111: 1200001 to 1549980 349980 bases
112: 1500001 to 1849980 349980 bases
113: 1800001 to 2272325 172325 bases"
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                               70.3%;
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1 (bases 1 to 1116)
Gilbert,M., Wakarchuk,W.W., Young,M.N. and Je
Recombinant alpha-2,3-sialyltransferases and
Patent: JP 2001503961-A 1 27-MAR-2001;
NATIONAL RESEARCH COUNCIL OF CANADA
OS Neisseria meningitidis
PN JP 2001503961-A/1
PD 27-MAR-2001
PF 10-JUN-1997 JP 1997526320
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2 (bases 1 to 1116)
Gilbert, M., Michniewicz, J.J.,
Direct Submission
Submitted (13-JUN-1996) Instit
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                                                            J. Biol.
8910446
                                                                                                    1 (bases 1 to 1116)
Gilbert,M., Watson,D.C., Cunningham,A.M., Jennings,M.P., Young,N.M.
and Wakarchuk,W.W.
Cloning of the lipooligosaccharide alpha-2,3-sialyltransferase from
the bacterial pathogens Neisseria meningitidis and Neisseria
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Neisseria meningitidis
Neisseria; Proteobacteria; Betaproteobacteria; Neisseriales;
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                                                                                         gonorrhoeae
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Neisseriaceae; Neisseria.
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Neisseria meningitidis
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JP 2001503961-A/1.
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Location/Qualifiers
   (13-JUN-1996) Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Neisseria meningitidis"
/mol_type="genomic DNA"
/db_xref="taxon:487"
                                                                                                                                                                                                                                                                                                        1116 bp DNA linear meningitidis alpha-2,3-sialyltransferase
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                              Watson, D.C. and Wakarchuk, W
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and their uses
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                                               Sequence update by submitter
On Dec 13, 1999 this sequence version
Location/Qualifiers
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Submitted (13-DEC-1999) Institute for Biological Sciences, National
Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario KlA
                                                                                                                                                                                                                   Direct Submission
Submitted (13-JUN-1996) Institute for Biological Sciences, National
Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario KlA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                3 (bases 1 to 1116)
Gilbert, M., Michniewicz, J.J.,
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J. Biol cr
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Cloning of the lipooligosaccharide alpha-2, 3-sialyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

1 (bases 1 to 1116)
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                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 271 (45),
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             organism="Neisseria meningitidis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MGLKKACLTVLCLIVFCFGIFYTFDRVNHGERNAVSLLKDKLFN EBGEFVNLIFCYTILOMKVAERIMAQHPGERFYVVLMSENRNEKYDYYFKQIKDKAER AYFFHLPYGLNKSFNFIFTMAELKVKSNLLFKVKRTYLASLEKVSIDAFLSTYPDAEI KTFDDGTGNLIQSSYLGDEFSVNGTIKRNFARMNIGDWSIAKTRNASDEHYTIFKGL KNIMDDGRRKWTYLFLFBASELKAGDBTGGTVRILLGSPDKEMKEISEKAAKNFNIQY VAPHPRQTYGLSGVTTLNSFYVIEDYILREIKKNPHTRYEIYTFFSGAALTMKDFPNV VAPHPRQTYGLSGVTTLNSFYVIEDYILREIKKNPHTRYEIYTFFSGAALTMKDFPNV VYALKPASLPEDYMLKPVYALFTQSGIPILTFDDKN"
mol_type="genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:6563405
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/protein_id="AAC44543.1"
/db_xref="GI:1546007"
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/strain="406Y, NRCC 4030"
/db_xref="taxon:487"
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Pred. No.
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Cloning of the lipooligosaccharide alpha-2,3-sialyltransferase from the bacterial pathogens Neisseria meningitidis and Neisseria
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-JUN-1996) Institute for Biological Sciences, National Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario KIA
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Gilbert M., Michniewicz, J.J., Watson, D.C. and Wakarchuk, W.W.
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8910446
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/trānslation="mslkkacltvlclivfcfgifytfdrvnhgernavsllkdklfn
EEGEPVNL1FCYTILOMKVAERIMAQHPGERFYVVLMSENRNEKYDYYFKQIKDKAER
AYFFHLPYGLNKSFNFIPTMAELKVKSMLLPKVKRIYLASLEKVSIAAF"
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/strain="M982B, NRCC 4725"
/db_xref="taxon:487"
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /traibilation="MGLKKACLTVLCLIVFCFGIFYTEDRVNQGERNAVSLLKDKLFN EEGEBVNLIFCYTILOMKVABRIMAOHPGERRYVVLMSENRNEKYDYYFNQIKDKAEW AYFFHLPYGINKSFNIFTMAELKVKAMLLFKYTYLASLEKYSIAAFLSTYPDAEI KTEDDGTINLIGSSSYLGDEFSVNGTIKRNEADHOTILLGSPDKEMKEISEKAAKNFNIQY KNIMDDGRRKMTYLFLFDASELKAGDETGGTVRILLGSPDKEMKEISEKAAKNFNIQY VAPHPROTYGLSGVTTLNSFYVIEDYLLREIKKNPHTRYEIYTFFSGAALTMKDFPNV
                                                                                                                                                                                        note="This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitidis truncated alpha-2,3-sialyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVYALKPASLPEDYWLKPVYALFTQSGIPILTFDDKN"
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/protein_id="AAC44544.2"
/db_xref="GI:6563406"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="126E, NRCC 4010"
/db_xref="taxon:487"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="Capsule type: C; lipooligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon
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Pred. No. 1.9;
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PROPRETED TO THE PROPRE	PCOMMENT  Sequence split into 308 fragments LO Fragment Name Begin End AP008212_000 1 11000  AP008217_001 100001 21000	Db 2 TGAGCTTGAAAAAGGCTTGTTTGACC 27  RESULT 14  AP008212_046/c	12 TGGGCTTGAAAAAGGCTTGTTTGACC	Query Match 65.9%; Score 24.4; DB 15; Length 1115; Best Local Similarity 96.2%; Pred. No. 10; Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	ORIGIN
	08212_070 08212_071 08212_072 08212_073	212_065 212_066 212_067 212_068 212_069	212 062 212 063 212 064	08212 059 08212 060 08212 061	12_057
7500001 7600001 76000001 7710000 7710000 7710000 7710000 82100001 8210000 8210000 8410000 85100001 8610000 8610000 8610000 9110000 9210000	0001 711 0001 721 0001 731 0001 741	0001 661 0001 671 0001 681 0001 691	0001 631 0001 641 0001 651	0001 601	0001

4 TGGAATTCTGGGCTTGAAAAAGGCTTGTTTGACC 37	Query Match 65.9%; Score 24.4; DB 4; Length 110000; Best Local Similarity 82.4%; Pred. No. 7; Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;		19200001	18900001 19000001	18700001 18800001	18500001	18200001 18300001	18000001	17800001	17500001	17300001 17400001	17100001 17200001	16900001	16700001	16400001 1651000 16500001 1661000	16200001 1631000 16300001 1641000	16000001	15700001 15800001	15500001	15300001 15400001	15100001	14900001	14600001	14400001 14500001	14200001 14300001	14100001	13700001 13800001 13900001	000	13000001 13100001 13200001 13300001	
062 6200001 63 063 6300001 64	AP008210_058 5800001 5910000 AP008210_059 5900001 6010000 AP008210_060 6000001 6110000 AP008210_061 6110001 671000	8210_055     5500001     56       8210_056     5600001     57       8210_057     5700001     58	8210_052 5200001 53: 8210_053 5300001 54: 8210_054 5400001 55:	5000001 51 5100001 52	4800001 48 4800001 49	4500001 46 4600001 47	4300001 44 4400001 45	4000001 41 4100001 42 4200001 43	3800001 39 3900001 40	3600001 37 3700001 38	3400001 35 3500001 36	3200001 33	3100001 30	7 2700001 28 2800001 29	2500001 26 2600001 27	2300001 24 2400001 25	2000001 21	1800001 19 1900001 20	1600001 17 7 1700001 18	1400001 15 1500001 16	1100001 12 2 1200001 13	9 900001 10 1000001 11	7 700001 8 8 800001 9	500001 6	300001 4	1 100001 2 2 200001 3	eplit into 355 fragments	RESULT 15 AP008210 235/c WPCOMMENT	Db 16436 TGGAATGCAGGACTTGAAAAAGCTTTGGTTGACC 16403	

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Qy 4 TGGAAT        Db 11954 TGGAAT	Query Match Best Local Similarity Matches 28; Conser	AP008210_195 AP008210_196	AP008210_193 AP008210_194	AP008210_192	AP008210_190	AP008210_189	AP008210_10/	AP008210_186	AP008210 185	AP008210_183	AP008210_182	AP008210_180	. '7	AP008210_178	AP008210_176	AP008210_175	AP008210_174	AP008210_172	AP008210_171	AP008210_100	AP008210_168	AP008210_167	AP008210_166	AP008210_164	AP008210_163	AP008210_161	AP008210_160	AP008210_158	AP008210_157	AP008210_155 AP008210_155	AP008210_154	AP008210_153	AP008210_151	AP008210_150	AP008210 149	AP008210_147	AP008210_146	AP008210 145	AP008210 143	۰,	μ' 4.	1 'L	AP008210_138	AP008210_137
TCTGGGCTTGAA             GCAGGACTTGAA	65.9%; larity 82.4%; Conservative		10000				18800001	10000		18300001		18000001		17800001	17700001	17500001	17400001	17200001					16600001				ъ,						ىب د		10000			14500001		14200001	14100001	14000001	13800001	13700001
TGGAATTCTGGGCTTGAAAAAGGCTTGTTTGACC 37 	Score 24.4; DB 4; Length 110000; Pred. No. 7; 0; Mismatches 6; Indels 0; Gaps	19610000 19710000	19410000	19310000	19210000	19010000	18910000	18710000	18610000	18410000	18310000	18210000	18010000	17910000	17710000	17610000	17510000	17310000	17210000	17110000	16910000	16810000	16710000	16510000	16410000	16210000	16110000	16010000	15810000	15710000	15510000	15410000	15210000	15110000	15010000	14810000	14710000	14610000	14510000	14310000	14210000	14110000	13910000	13810000
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37
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

45	44		c 42			39	38	37	c 36	35	34	33	32			c 29		27	26	25	24	c 23	22	21	c 20	c 19
20.2	•	20.2	20.2	20.2	20.2	20.4	20.6	20.6	20.6	20.6	20.6	•	20.8	20.8	20.8	20.8	20.8	20.8	20.8	21.2	21.4	21.6			21.6	21.6
54.6	54.6	54.6			54.6	55.1	55.7	55.7	55.7	55.7	55.7		56.2	56.2	56.2	56.2	56.2	56.2	56.2	57.3	В	58.4		58.4	58.4	58.4
47307	3615	679	679	679	482	428	50720	946	660	404	404	217409	65277	2546	2546	2546	2546	1023	1022	455	114693	2482	2165	2017	1180	1096
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ADZ12798	ABQ70808	ADZ94693	ADU56690	AAF12649	ABZ54492	ACF86835	ABD33468	ADR64344	ACA48397	ADR64345	ADP93987	ACN45150	ABD32902	ADW80545	ADH75511	ABK17091	AAC62826	AAZ11768	AAZ11769	ACH38970	AAD48308	ADD48928	AAS68645	AAS80485	ADX64614	ADX35051
Adz12798 Murine ca	Abq70808 Listeria	Adz94693 Aspergill	Adu56690 Aspergill	Aaf12649 Aspergill	Abz54492 Aspergill	Acf86835 Human SIR	Abd33468 Murine ca	Adr64344 Cotton cD	Aca48397 Prokaryot	Adr64345 Cotton cD	Adp93987 Cotton ex	Acn45150 Human gen	Abd32902 Human can	Adw80545 Monterey	Adh75511 Pinus rad	Abk17091 Pinus rad	Aac62826 Male-spec	Aaz11768 Maize elo		Ach38970 Human foe	Aad48308 Human tra	Add48928 Human gen	Aas68645 DNA encod	Aas80485 DNA encod	Adx64614 Plant ful	Adx35051 Plant ful

### ALIGNMENTS

## AAX84284; AAX84284 standard; DNA; 37 ΒP

PCR primer for alpha-2,3-sialyltransferase coding sequence.

08-SEP-1999

(first entry)

Beta-1,4-galactosyltransferase; lgtB; fusion protein; catalytic domain; glycosyltransferase; accessory enzyme; nucleotide sugar formation; saccharide donor; oligosaccharide synthesis; alpha-2,3-sialyltrnsferase; carbohydrate structure development; PCR primer; ss.

RESULT 1
AAXX64264
IID AAXX6
IID AAXX6
XX AAXX6
XX AAXX6
XX Beta
XX Beta
XX Beta
XX Synt
CS Sy 15-DEC-1997; 14-DEC-1998; 15-DEC-1998; 24-JUN-1999 WO9931224-A2 Neisseria sp. Synthetic (CANA ) NAT RES COUNCIL CANADA. 97US-0069443P. 98US-00211691. 98WO-CA001180

Gilbert M, Young NM, Wakarchuk WW;

A new glycosyltransferase fusion protein useful in the enzymatic synthesis of oligosaccharides.

WPI; 1999-395174/33.

Example 1; Page 40; 63pp; English.

This sequence represents a PCR primer for the Neisseria alpha-2,3-sialyltransferase coding sequence. The invention relates to a nucleic acid encoding a fusion protein that comprises a glycosyltransferase

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catalytic domain and a catalytic domain from an accessory enzyme that is cinvolved in formation of a nucleotide sugar which is a saccharide donor great a glycosyltransferase reaction. The fusion protein is useful in the catalyse more than one reaction involved in the enzymatic synthesis of oligosaccharides. The fusion proteins are able to is useful for the development of therapeutic agents that have specific catalyse more than one reaction involved in the enzymatic synthesis. This cc carbohydrate structures. Carbohydrates are involved in recognition cc synthesis of the surface of cells. The fusion protein can be used for the coverless of both natural carbohydrates and synthetic derivatives with convel properties. The fusion polypeptide allows two glycosyltransferase cc reactions in a single vessel, provides improved yields of end products. Cc reduced. The fusion protein can also use directly different donor canalogues and various acceptors with a terminal galactose residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches 37
   The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AABS25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
                                                                                                                                     Claim 7; Page 1385-1390;
                                                                                                                                                                      Neisserial infections,
                                                                                                                                                                         Isolated nucleotide sequences of Neisseria meningitidis which in the diagnosis and treatment of N. meningitidis infection are
                                                                                                                                                                                                                                                                              Frazer CM, I
                                                                                                                                                                                                                                                                                                                                                      09-OCT-1998;
30-APR-1999;
                                                                                                                                                                                                                                  WPI; 2000-318079/27.
                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis; Neisseria gonorrheae; genome; antigen; vaccine; diagnosis; infection; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. meningitidis partial DNA sequence gnm_62 SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200022430-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meningococcus B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATGGAATTCTGGGCTTGAAAAAGGCTTGTTTGACC
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99US-0132068P
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                                                                                                                                  1760pp; English.
polynucleotide
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Ratti G, Scarselli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunogenic;
; identification;
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ORF sequences,

which are

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AC AAF2
AC AAF2
XX
DT 13-M
XX
Neis
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Neis
XW
Neis
XW
diag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc used in the exemplification of the present invention. The nucleic acid cc sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a cc medicament (or in the manufacture of a medicament) for treating, cc example, some of the identified proteins could be components of vaccines cc against Meningococcus B; against all serotypes; and/or against all cc against Meningococcus B; against all serotypes; and/or against all cc against Meningococcus B; against all serotypes; and/or against all cc against meningococcus B; against all serotypes; and/or against all cc against meningococcus B; against all serotypes; and/or against all cc against meningococcus B; against all serotypes; and/or against all cc against meningococcus B; against all serotypes; and/or against all cc against septicitic probes. Attempts to make efficacious Meningococcus B cracines have failed mainly due to antigen tolerance. Multivalent cc vaccines have also been tried but none have successfully overcome creations are not considered an opportunity to identify secreted or surface exposed proteins continued by the presumed targets for the immune system and which are not considered to antigenically variable or at least more conserved than other more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                       Neisseria meningitidis;
diagnosis; antigen; det
                                                            Neisseria meningitidis B nucleotide sequence SEQ ID NO:110
                                                                                                      13-MAR-2001
                                                                                                                                       AAF21609;
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split into
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                                                                                                                                                               standard; DNA; 349980
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                                                                                                                                                                                                                                                                  TCTGGGCTTGAAAAAGGCTTGTTTGACC
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                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                  (first entry)
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             is; Neisseria gonorrheae; immunogenic; vaccine; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                  1200001
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Pred. No. 1
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RRESULT 5
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     computer storage medium or computer databases can be used in a search to identify open reading frames (ORTS) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Appendix A; 692pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis B full length frames are used to detect, treat and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pizza w,
Masignani V, Galeutte
Pi R, Frazer CM,
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                                                                                                                                                              AAF21608;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 349980
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08-OCT-1999;
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                                 diagnosis;
                                                  Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine;
                                                                                    Neisseria meningitidis B nucleotide sequence SEQ ID NO:109
                                                                                                                          13-MAR-2001
                                                                                                                                                                                            AAF21608 standard; DNA; 349980
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                                antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                        (first entry)
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99WO-US023573
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otti C, Mora M,
r CM, Grandi G;
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96.4%;
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Pred. No. 2.
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, Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome sequence and open reading prevent Neisserial infections.
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Scarselli M,
                                                                                                                                                                                                                                                                                                                                                           1;
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RESULT 6
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AAV0
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AC AAV0
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DT 17-0
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KW Alph
KW Alph
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OS Neig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC represent fragments of the NMB genomic sequence, as the sequences which coverlap each other at the beginning and end of each sequences which coverlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of CC (AAF21607, the last 49980 bp of AAF21547 are repeated at the beginning of CC AAF21607, the last 49980 bp of AAF21545 to AAF21588 encode the Neisseria proteins CC given in AAB5859 to AAF21545 to AAF21588 encode the Neisseria proteins CC given in AAB5859 to AAF21545 to AAF21588 encode the present pCR primers which are used in the exemplification of the present invention. CC The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisseria nucleic acids, proteins CC and/or antibodies which binds to the proteins can be used in compositions CC for treating or preventing infection due to Neisserial bacteria or as a CC diagnostic reagent for detecting the presence of Neisserial bacteria or cc of antibodies raised to Neisserial bacteria. Computers can be used in a search to computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB counter memory. The DNA sequences provide further opportunities to find antigenic content memory are contains which are more effective in vaccines than the
                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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Masignani V, Galeotti c
                                                                                           N. meningitidis alpha-2,3-sialyltransferase
                                                                                                                                   17-JUN-1998
                                 Alpha-2,3-sialyltransferase; sialic acid; acceptor; lipid; biologically active oligosaccharide; sialyl-modified protein; ss.
                                                                                                                                                                       AAV04125;
                                                                                                                                                                                                           AAV04125 standard; DNA; 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Appendix A; 692pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 outer membrane proteins currently used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
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08-OCT-1999;
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V, Galeotti C, Mora M,
R, Frazer CM, Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                               (first entry)
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99WO-US023573.
                                                                                                                                                                                                                                                                                                                                                                                                    96.4%;
                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 2.
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, Ratti G,
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Scarselli M,
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Neisseria meningitidis.

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ACC XXX DEXXXX DEXXXX DEXXXX DEXXXX DEXXXX DEXXX DEXXX
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AAH07120
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Best Local
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           29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                   28-JUL-2000;
                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                     EP1074617-A2
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                  AAH07120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes an alpha-2,3-siallyltransferase which has been isolated from Neisseria meningitidis. The protein can be used as a reagent for adding a sialic acid residue to an acceptor having a terminal galactose residue, e.g. in synthesis of biologically active oligosaccharides or sialyl-modified proteins or lipids. The nucleic acid sequence can be used for the recombinant production of alpha-2,3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 199
P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid sequence encoding Neisseria alpha-2,3-sialyl:transferase useful to add sialic acid to acceptor with terminal galactose residue synthesis of biologically active oligosaccharide.
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07-JUN-1997;
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                                                                                                                                                                                                                                                                                cDNA clone (5'-primer) SEQ ID NO:3955.
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                                                                                                                                                                                                                                                          primer;
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       ; 99JP-00248036.
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; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
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97US-00872485.
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/product= "alpha-2,3-sialyl transferase"
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Pred. No.
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CC nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination (c) of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination (c) of an oligonucleotide comprising a sequence complementary to the comprises at least 15 nucleotide which comprises a 5'-end (c) sequence and an oligonucleotide comprising a sequence complementary to a coligonucleotide which comprises a 1'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of complementary to a coligonucleotide comprises at least 15 nucleotides and the combination of complementary. The primer sets can be used in antisense therapy and in the complementary to a coligonucleotide comprises are useful for synthesising polynucleotides, complementary to a coligonucleotide comprises are useful for synthesising polynucleotides, complementary and in the complementary and in the complementary and in complementary to a complementary to a complementary to a complementary and in the selected from those defined in the complementary and in the complementary to a comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602
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Ishii S,
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sugiyama
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T, Wakamatsu A,
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A, Nagai K,
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C, Otsuki
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RESULT 8
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AC ABL190
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                                                                 23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; pharmaceutical; gene; ds.
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83.9%;
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Pred. No. 1
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); Mismatches
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Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL016176) and the encoded proteins (ABL01737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                    Tang YT,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; genome mapping; gene therapy; food supplement; virus; cell-proliferative disorder; neurodegenerative disease; bacte Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; multiple sclerosis; diabetes; genetic disorder; wound; burn;
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                                                                                                                                                     Yang Y, Ma
T, Wang J,
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                                                                                                                                                                                                                                                                    HYSEQ INC
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                                                                                                                                                        Goodrich RW, Asundi V,
Ma Y, Yamazaki V, Chen
, Wang D, Drmanac RT;
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77.8%;
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Pred. No. 19;
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, Ghosh !
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New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative,

Disclosure;

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for diagnosing and/or t ty of the arginine-rich

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAR-2001; 2001US-00799451
05-MAR-2002; 2002WO-US005095
20-AUG-2002; 2002US-00225251
                                                                                                                New isolated arginine-rich protein-like polynucleotides and polypeptides, useful for diagnosing and/or treating conditions associated with aberrant activity of the arginine-rich polypeptides, such as cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2002; 2002US-00302172
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genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
                                                                                                                                                                                                                                          WPI; 2004-238579/22
                                                                                                                                                                                                                                                                                                                                                           (TANG/) TANG Y T.
(XUEA/) XUE A.
(DRMA/) DRMANAC R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABZ12066) or their mature protein coding portion, active domain coding
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                                                                                                                                                                                                                                                                                               Xue A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arginine-rich protein; cancer; inflammation;
                                                                                                                                                                                                                                                                                                  Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selected from any of
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Pred. No.
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22;
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RESULT 11
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Best Local S
Matches 26
length cDNAs defined in the specification, where a primer sets comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 oligonucleotide sequences defined in the specification, where the of an oligonucleotide comprising a sequence complementary to the sequence of an oligonucleotide comprising a sequence complementary to the sequence complementary strand of a polynucleotide which comprises a 5'-end polynucleotide which comprises a 5'-end polynucleotide which comprises a 5'-end sequence complementary to a oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 3'-end sequence, where the oligonucleotide comprises a 1-end sequence, where the strend sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in
                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                  The present invention
                                                                                                                                                                                                                 Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-1999;
27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH16361 standard; cDNA; 2228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polynucleotide. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with aberrant expression or activity of the arginine-rich protein-like polypeptides, such as mapping, identification of mutations responsible for genetic disorders, and in assessing bloddyersity. The present sequence represents a novel
                                                                                                                                                                                                                                                                                                                                                                                               (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                    Isogai T,
Sugiyama
                                                                                                                                                                                                   SEQ ID NO 15295; 2537pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence SEQ ID NO:15295.
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2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
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T, Wakamats
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                                                                                                                                                                       describes primer sets for synthesising
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Wakamatsu A, Nagai K,
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Pred. No. 22;
0; Mismatches
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C, Otsuki
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T;
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The present invention describes an isolated tumour-associated antigenic CC trarget (TAT) nucleic acid comprising: (a) any of 4622 nucleotide CC sequences (see SEQ ID No:1 to 4622); (b) the full-length coding region of CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80% CC (c). Also described: (l) an expression vector comprising the above (c) nucleic acid; (2) a host cell comprising the above expression vector; (3) CC a process for producing a polypeptide; (4) an isolated polypeptide CC nucleotide sequences; (b) an amino acid sequence encoded by any of the above CC nucleotide sequences; (b) an amino acid sequence encoded by the full-CC length coding region of the above nucleotide sequences; or (c) a sequence (c) at least 80% identical to (a) or (b); (5) a chimeric polypeptide; (6) CC comprising the above polypeptide fused to a heterologous polypeptide; (6) a soluted antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide (7AT)
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ADQ84099
ID ADQ84
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Matches 26
                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 913; 5504pp; English.
                                                                                                                                                                                                                                                                                                          New nucleic acid molecule and encoded polypeptide, i preventing or treating cell proliferative disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; tumour-associated antigenic target; cancer; cell proliferative disorder; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2003; 2003WO-US029126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                 (/UOHZ)
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ZHOU Y.
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WU T D.
                                                                                                                                                                                                                                                                                                                                                                                                Zhou Y;
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26; Conserv
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                                                                                                                                                                                                                                                                                                                         diagnosing,
                                                                                                                                                                                                                                                                                                             as cancer
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(TAT)
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RESULT 13
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; SECP; neurodegenerative disorder; scleroderma; Parkinson's disease; Alzheimer's disease; myotonic dystrophy; leukaemia; muscular disorder; systemic lupus erythematosus; renal disorder; cancer; immunological disorder; gastrointestinal disorder; catatonia; infection; diabetes; Goodpasture's syndrome; cardiovascular disorder; gene therapy; endocrine disorder; atherosclerosis; transgenic animal; Grave's disease;
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                                                             28-NOV-2001; 2001US-0334229P
07-DEC-2001; 2001US-0339236P
21-DEC-2001; 2001US-0343553P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL61230 standard; cDNA; 2942
                                                                                                                                                                                                           21-NOV-2002; 2002WO-US037803
                                                                                                                                                                                                                                                                                                                                                     WO2003046196-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
(INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAT cDNA sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAATTCTGGGCTTGAAAAAGGCTTGTTTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2228 BP; 663 A; 460 C; 475 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAACTTCTGGGCTTTAAAAAGACTTGCTTGA 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein (SECP) -1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease; hepatic disease;
                                                                                                                                                                                                                                                                                                                                                                                                               product= "Human SECP protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        630 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cirrhosis; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ű
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 Other;
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밁 Ş

Baughn MR,

Becha SD,

Chawla NK,

Emerling

ВМ,

Fu

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Ison

9

New isolated nucleic acid segments from the human genome - used

for

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AAX10673/c
ID AAX106
XX AAX106
XX AAX106
XX JO-MAR
XX Human
XX POlymo
KW POlymo
KW Autoim
KW Autoim
XX Homo s
XX Homo s
XX WO9820
XX WO9820
XX PD 14-MAY
XX PF 05-NOV
XX PF 06-NOV
XX PR 06-NOV
XX PR WHED
XX WHED
XX WHED
XX WHI; 1
XX WPI; 1
XX New is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkinson's disease, Altheimer's disease), muscular disorders (e.g. myotonic dystrophy, catatonia), endocrine disorders (e.g. diabetes, Carave's disease), cancers (e.g. leukaemia, cervical or breast cancers), immunological disorders (e.g. scleroderma, systemic lupus erythematosus, allergies), gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's syndrome) infections (e.g. viral, fungal, bacterial, parasitic, protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis) or hepatic diseases (e.g. cirrhostis). SECP polynucleotides can be used to create humanised animals or transgenic animals to model human disease. The invention is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecules encoding such proteins. SECP sequences are useful in diagnosing, preventing and treating disorders associated with an at expression or activity of SECP such as neurodegenerative disorders
                                                                                                                                                            05-NOV-1997;
                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                   Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                  Human biallelic
                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX10673
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX10673 standard; DNA; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human secreted proteins (SECP) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and/or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New SECP polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, e.g. neuromuscular, immunological, cardiovascular disorders, cancer
                                WPI; 1998-286974/25
                                                                                                                             06-NOV-1996;
                                                                                                                                                                                           14-MAY-1998
                                                                                                                                                                                                                         WO9820165-A2
                                                                                                                                                                                                                                                                                   treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ramkumar
                                                                                             (WHED ) WHITEHEAD INST BIOMEDICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is human SECP protein encoding cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kable AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAACTTCTGGGCTTTAAAAAGACTTGCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAATTCTGGGCTTGAAAAAGGCTTGTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2942 BP; 883 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 170-171; 194pp;
                                                                                                                                                                                                                                                                                                  phenotypic typing; disease; cancer; ir
                                                             Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Richardson
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                             96US-0030455P
                                                                                                                                                            97WO-US020313
                                                                                                                                                                                                                                                                                                                                                                polymorphic DNA fragment WI-6315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.2%;
83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PG,
TW,
Das
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      624 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ö
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Swarnakar A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 24;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       656 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marquis JP, Lel
kar A, Tran UK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lehr-Mason
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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RESULT 15
AAX10672/c
ID AAX10672 standard; DNA; 225 BP
XX
AC AAX10672;
XX
DT 30-MAR-1999 (first entry)
XX
POlymorphism; biallelic; human
KW detection; phenotypic typing;
KW autoimmune disease; cancer; in
XX
POLYMORPHISM; marker; ss.
XX
WO9820165-A2.
XX
PN WO9820165-A2.
XX
OS Homo sapiens.
XX
PN WO9820165-A2.
XX
PF USCOUNTING SECULOUS SECULOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX10269-X12937 are human DNA fragments which contain biallelic CC polymorphic markers which have been isolated using the primers CC represented in AAX09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments CC can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, will be and's disease, tuberous sclerosis, hereditary CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary CC syndrome, osteogenesis imperfecta, acute intermittent porphyria, CC syndrome, osteogenesis imperfecta, acute intermittent porphyria, CC system, infection by pathogenic microorganisms, and characteristics such endurance, fertility, and susceptibility or receptivity to particular CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or vy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                         New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human biallelic polymorphic DNA fragment WI-6315b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 70; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                              1; Page 70; 310pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Н
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27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCATGACACGCTGGGCTTGAAAAGGGACTGTTTG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCATGGAATTCTGGGCTTGAAAAAGGCTTGTTTG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.6%;
79.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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CC AAX10269-X12937 are human DNA fragments which contain biallelic CC polymorphic markers which have been isolated using the primers CC represented in AAX09121-X10268. The base occupying the polymorphic site CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments CC can be used in methods for determining polymorphic forms in an individual CC for use in e.g. forensics, patermity testing or for phenotypic typing for CC diseases such as agammagloblinemia, diabetes insipidus, Lesch-Nyhan CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary CC spherocytosis, von Willebrand's disease, tuberous selerosis, hereditary CC syndrome, osteogenesis imperfecta, acute intermittent porphyria, CC syndrome, osteogenesis imperfecta, acute intermittent porphyria, CC system, infection by pathogenic microorganisms, and characteristics such CC as longevity, appearance (e.g. baldness, obesity), strength, speed, CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid CC coronbylaxis of such diseases
Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                     Sequence 225 BP; 55 A; 50 C;
                                                                                                                                    prophylaxis of such diseases
                 61.6%;
79.4%;
                   Score 22.8;
Pred. No. 1
                                                                                     46 G;
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                                                                                   Other;
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Search completed: May 19, Job time : 180.906 secs 2006, 00:53:17

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Gapop 10.0 , Gapext 1.0
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37
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   GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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 CR109858
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AZ192473 SP 1021 B
BI096984 SCUM3-DS
BF744479 QV2-BT063
CG614466 OST302754
DB047668 DB047668
DB021107 DB021107
CG59353 OST258118
DB056413 DB056413
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C80222 C80292 Mous
CL969122 OSIFCC017
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BB642392 BB642392
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BX103153 BX103153	T15936 IB2156 Infa	Z38338 HSC07B032 n	AK033409 Mus muscu	AK029724 Mus muscu	AK020021 Mus muscu	AK044441 Mus muscu	AK037169 Mus muscu	AY404518 Pan trogl	AY404517 Homo sapi	AY404519 Mus muscu	CD632278 56049046H	CR040392 Forward s	BG771738 602720406	CJ488602 CJ488602	BB615455 BB615455	BY717855 BY717855	BG773112 602721833	BB617250 BB617250	CV024531 1931 Full	DB031132 DB031132	DB039479 DB039479	AW962292 EST374365	DB031260 DB031260		DB049403 DB049403

### ALIGNMENTS

FEATURES SOUTCE		TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AI325176/c LOCUS DEFINITION
This clone was previously sequenced on the 5' end only, this new data is from the 3' end High quality sequence stop: 432. Location/Qualifiers 1901 /organism="Mus musculus" /mol_type="mRNA" /db xref="taxon:10090" /clone="IMAGE:605735" /tissue_type="carcinoma"	Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. The WashU-HHMI Mouse EST Project Unpublished (1996) Contact: Marra M/Mouse EST Project	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  1 (bases 1 to 901) Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,	Al325176.1 GI:4059605 EST. Mus musculus (house mouse) Mus musculus	AI325176 901 bp mRNA linear EST 23-DEC-1998 ms01h12.x1 Stratagene mouse embryonic carcinoma (#937317) Mus musculius cDNA clone IMAGE:605735 3' similar to gb:D16141 Mouse mol-1 mena for OPF Complete of (MOUSE). mRNA segmente

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ACCESSION ', VERSION
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CL969122
LOCUS
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CL969122 1443 bp DNA linear GSS
OSIFCC017869 Oryza sativa Express Library Oryza sativa
Cultivar-group) genomic, genomic survey sequence.
CL969122
CL969122.1 GI:52392873
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Contact: Hirofumi Doi
Doi Bioasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hd@bioa.jst.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Systematic analyses of genes expressed in 3.5-dpc (The ERATO/Doi Project at Wayne State University)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murcidee; Muridae; Murinae; Mus.

1 (bases 1 to 618)

KO,M.S.H., Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T., Grahovac,M.J., Mason,S., Lim,M.K., Paonessa,P.D., Sauls,A.D. and Doi,H.
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C80292 C80292 Mouse 3.5-dpc blastocyst cDNA Mus musculus cDNA clone J0079C07 3' similar to Human mRNA for KIAA0312 gene, mRNA sequence.
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                                                                                                                                                                                                                                                                                                        /tissue_type="blastocyst"
/dev_stage="3.5-dpc"
                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="J0079C07"
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. PT9 . line. Average insert size: 1.0 kb; Uni-Zap XR Vector; adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                      clone_lib="Mouse 3.5-dpc blastocyst cDNA"
                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev stage="embryonic"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse embryonic
(#937317)"
                                                                                                                                                                                                                             68.6%;
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81.1%;
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Pred. No. 22;
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GSS.
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Fax: 86-10-80488676
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Oxyza sativa (indica cultivar-group)
Oxyza sativa (indica cultivar-group)
Oxyza sativa (indica cultivar-group)
Oxyza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 1443)
1 (bases 1 to Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Thao. H., Yuan, L.,
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences,
Tel: 86-10-80481559
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                                                                                                                                                                                                                                                                                                    Email: chenchen@genomics.org
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing
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An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
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/organism="Oryza sativa
/mol_type="genomic DNA"
                                                                                                                                                     Location/Qualifiers
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/mol type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express
/note="Oryza sativa exon trapped
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Pred. No. 70;
0; Mismatches
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و
                                 cultivar-group) "
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arakawa T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB642392 RIKEN full-length enriched, adult retina Mus musculus cDNA
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                                                                                                                                                                                                                                                                                                                         Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) waggi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Watsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                    Human Genome Sequences. Mamm.
                                                                                                                                                                                                                encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KOndo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
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                                                                               Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                           Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Hayashizaki,Y.
                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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/clone_lib="Oryza sativa
/note="Oryza sativa exon
                    Location/Qualifiers
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Pred. No. 70;
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RESULT 6
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Best Local
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                                                                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
CF295692
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
                                                                                                                                                                                                                                           Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF295692 635 bp mRNA linear 30DGS--05-L22.gl Rice leaf plasmid cDNA library I
                                                                                                                                        Email: bhnahm@ggbio.com,
                                                                                                                                                      Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                 Contact: Nahm B.H
                                                                                                                                                                                                                                                                                                                          clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                   CF295692.1 GI:33664725
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/db xref="taxon.39947"
/clone="30DGS--05-L22"
/tissue_type="leaf"
/dev_stage="30 days afte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                       Location/Qualifiers
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/db_xref="taxon:10090"
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lab_host="DH10B"
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                                                                                                                                                                                      Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24;
Pred. No.
    days after germination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                      bhnahm@bio.myongji.ac.kr
                                                                                            (japonica cultivar-group)"
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د.
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SOURCE
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                                                                         REFERENCE
AUTHORS
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VERSION
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CR207976
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CR109858
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            Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 843)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Rogers, J. and Bradley, A. Direct Submission
Submitted 100
                                                                                                                                                                                                                                                                                                                   656 GCATGGAATTCTGTGTTTGAAATAATATCGTTTGA 690
                                                                                                                                                                                   CR207976.1 GI:49986825
                                                                                                                                                     GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
                                                                                                                                                                                                           chromosome engineering clone MHPN184k16, genomic
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Forward strand read
                                                                                                                                                                                                                                                                                                                                          1 GCATGGAATTCTGGGCTTGAAAAAGGCTTGTTTGA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (20-FEB-2004) Sanger Centre, Hinxton, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rogers, J. and Brac
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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   (20-FEB-2004) Sanger Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN180924"
/clone_lib="MHPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E.coli DH10B" /clone lib="Rice leaf plasmid cDNA library I (30DGS)" /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                             64.3%;
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80.0%;
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Pred. No. le+02;
0; Mismatches
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   Hinxton,
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Nishijima,I., y
Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cambridgeshire,
                                                                                                                                                                                                          survey sequence.
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                                          Yu, Y.,
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         AUTHORS
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DEFINITION
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CR050996
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AUTHORS
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VERSION
KEYWORDS
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CR126869
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Best Local S
Matches 28
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Best Local :
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                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Euarchontoglires; Glires; Rodent Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 912)
                                                                                                                                                        CR050996
CR050996.1
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                                                                                                                                                                              CR050996 912 bp DNA linear GSS 05-JUL-20. Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN71g17, genomic survey sequence.
   Adams,D.J., Biggs,P.J., Cox,A.V., Jonkers,J., Smith,J., Plumb,R.W.,
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                                                                                                                                                                                                                                                                                                                                                                               28;
                                                                                                                   GSS; genome survey sequence; MICER. Mus musculus (house mouse)
                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (20-FEB-2004) Sanger Centre, CB10 ISA, UK. http://www.sanger.ac.uk/Location/Qualifiers
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ROTWARD Strand read from insert in 5'HPRT insertion targeting and Chromosome engineering clone MHPN78a07, genomic survey sequence. CR126869

CR126869

CR126869. GI:49874321

GSS: genome survey sequence; MICER.

Mus musculus (house mouse)

Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN78a07"
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/db_xref="taxon:10090"
/clone="MHPN184k16"
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80.0%;
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80.0%;
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Pred. No. 1.1e+02;
0; Mismatches 7;
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Pred. No. 1.1e+02;
   Davies,R.M.,
Taylor,R.G.,
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                                                                 Rodentia;
van der Weyder
Nishijima,I.,
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Nishijima,I., Y
                                                                                                                                                                                                                                                                                                                                                                                                    884;
                                                                               Euteleostomi;
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         Matches
                         Best Local Similarity
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Direct Submission
Submitted (20-FEB-2
CB10 1SA, UK. http:
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Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M. Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
AU133964
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AU133964 OVARC1 Homo sapiens
                                                                                                                                                                                                                                                             Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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                                                                                                                                                                                                                                                                                                                                                               Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                      FLJ Project (HRI Team)
Helix Research Institute
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Genome Res. 16 (1), 55-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens (human)
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       Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN71g17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                /clone_Tib="OV/
/note="Vector:
                                                                                                                   tissue_type="ovary, tumor tissue'/clone_Tib="OVARC1"
                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="MHPN"
                                                                                                                                                       clone="OVARC1001010"
                                                                                                                                                                         'mol_type="mRNA"
'db_xref="taxon:9606"
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                         63.8%;
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Pred. No. 1.1e+02;
0; Mismatches 7;
     Score 23.6; DB 1;
Pred. No. 1.3e+02;
0; Mismatches 5;
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5;
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                                         Length 726;
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     Gaps
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ACCESSION
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AZ192473

P1021 B1 E08 SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm Genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1021 Col=15 Row=J, genomic survey sequence. AZ192473
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                                                        Melaleuca alternifolia (tea tree)
Melaleuca alternifolia
                                                                                                                                                                    BI096984 663 bp r
SCUM32-DS1-1 Melaleuca alternifolia
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                                                                                                                                                                                                                                                                                                                                                                      27;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Myrtales; Myrtaceae; Melaleuca.
                                                                                                                                     BI096984
                                                                                                                                                   alternifolia cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: SP6
Class: BAC ends
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Plate: 1021 row: J column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 97 (17), 10920195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A sea urchin genome project: Sequence scan, virtual map,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. and Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T.,
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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Fax: (626) 793-3047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="plate=1021 Col=15 Row=J"
/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Strongylocentrotus purpuratus'
/mol_type="genomic DNA"
/db_xref="taxon:7668"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
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                                                                                                                                                     mRNA
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Pred. No. 1.6e
0; Mismatches
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1 (Cheel) mRNA Melaleuca
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                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo.

1 (bases 1 to 453)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Shotgun sequencing of the human transcriptome with ORF expressed Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-BT0636-
291000-443-a01&t3=2000-10-29&t4=1)
                                                                                                                                                                                                                                                                                                      Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
                                                                                                                                                                                                                                                                Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCATGGAATTCTGGGCTTGAAAAAAGGCTTGTTTGACC 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
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EST.
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QV2-BT0636-291000-443-a01 BT0636 Homo sapiens cDNA,
BF744479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Southern Cross University
P.O. Box 157, Lismore, NSW 2480, Australia
Tel: 61 2 6620 3173
Fax: 61 2 6622 2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shelton, D., Leach, D., Baverstock, P and Henry, R.
Isolation of genes involved in secondary metabolism from Melaleuca alternifolia (Cheel) using expressed sequence tags (ESTs) Plant Sci. 162 (1), 9-15 (2002)
Contact: Shelton D
Centre for Plant Conservation Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Location/Qualifiers
                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                                                     Location/Qualifiers
                 clone_lib="BT0636"
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/mol_type="mRNA"
/db_xref="taxon:164405"
/clone_lib="Melaleuca alternifolia (Cheel) mRNA"
                                                                                                         .453
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Pred. No. 1.9e+02;
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Zambrowicz, B. P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Pigott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Priddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

Which kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands,
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE
described in Zambrowicz et al (Nature. 1998
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                                                                                                                          Similarity
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GAACTTCTGGGTTTTAAAAAGACTTGTTTGA 438
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CG614466.1 GI:37438315
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/db_xref="taxon:10090"
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/clone_lib="Mus musculus 129Sv/Ev"
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                                                                                                                     62.2%;
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Pred. No. 2.1e+02;
0; Mismatches 5
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1998 Apr 9;392(6676):608-11)
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6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/P_COMB.seq:*

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Sequence 13003, A
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153, App	3813, Ap	1435, Ap	261, App	1, Appli	<ol> <li>Appli</li> </ol>	140222,	140221,	34057, A	34056, A	15779, A	15790, A	13968, A	51, Appl	<ol><li>Appli</li></ol>	3, Appli	28576, A	18901, A	3, Appli	14158, A	12510, A	191, App

### ALIGNMENTS

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CLASSIFICATION: 435	٠.
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STATE: California	••
San Francisco	٠.
vo Embarcadero Center, Eighth Flo	<b></b> .
ADDRESSEE: Townsend and Townsend and Crew LLP	
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OF INVENTION: and Their Us	٠
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Jennings,	<b></b> .
Wakarchuk	٠
APPLICANT: Gilbert, Michel	
	<b></b> .
Patent No. 6096529	
Sequence 1. Application US/08872485	. ;
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IOCATION: CDS
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ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,942
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US-09-387-942-1
                                                                                                                                                                                                                    NAME: Smith, Timothy L.

REGISTRATION NUMBER: 35,367
REFERENCE DOCKET NUMBER: 0141:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1116 base pairs
TYPE: DOCKET NUMBER: 0116
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                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Smith, Timothy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gilbert, Michel APPLICANT: Wakarchuk, Warren W. APPLICANT: Young, N. Martin APPLICANT: Jennings, Micheal P. TITLE OF INVENTION: Recombinant TITLE OF INVENTION: and Their U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
        LOCATION: 1..1116
OTHER INFORMATION:
                             NAME/KEY: CDS
LOCATION: 1..
                                                                  ORGANISM: Neisseria meningitidis
STRAIN: 406Y, NRCC 4030
INDIVIDUAL ISOLATE: Capsule type
INDIVIDUAL ISOLATE: type: L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 LENGTH: 1116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two CITY: San Francisco
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STRAIN: 4067, NRCC 4030
INDIVIDUAL ISOLATE: Capsule type:
INDIVIDUAL ISOLATE: type: L3
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                                                                                                                                                                     linear
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                                                                                                                                                         DNA (genomic)
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/product= "alpha-2,3-sialyltransferase"
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                                                                    Capsule type:
type: L3
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Pred. No.
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                                                                               Y; lipooligosaccharide
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                              RESULT 4
US-09-949-016-15676/c
                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
; NAME/KEY: CDS
; LOCATION: (208)...(1695)
US-09-799-451-243
                                                                                                                                                                     Sequence 15676, Application US/09949016 Patent No. 6812339
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Best Local
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CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt FL genes Version 2.0
SEQ ID NO 243
LENGTH: 1734
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Best Local Similarity 100.
26; Conservative
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TITLE OF INVENTION: No. 6783969el Nucleic Acids
TITLE OF INVENTION: Polypeptides
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APPLICANT:
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APPLICANT: Tang, Y. Ton
APPLICANT: Zhou, Ping
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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26; Conserva
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Yang, Yonghong
Wehrman, Tom
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Ma, Yunging
Yamazaki, Victoria
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Ghosh, Reena
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Xue, Aidong J.
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Wang, Jian-Rui
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Asundi, Vinod
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Zhiwei
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TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(62873)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15676
Sequence 5, Application US/09257584A
Patent No. 6177611
GENERAL INFORMATION:
APPLICANT: Rice, Douglas A.
TITLE OF INVENTION: Constitutive Maize Promoters
FILE REFERENCE: 5718-33, 035718/175218
CURRENT APPLICATION UMMBER: US/09/257,584A
CURRENT FILING DATE: 1999-02-25
EARLIER FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 15676
LENGTH: 62873
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Best Local
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Best Local
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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Pred. No. 1.3e+02;
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Pred. No. 1e+02;
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 2546
TYPE: DNA
ORGANISM: Pinus radiata
US-09-598-401C-95
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US-09-598-401C-95/c
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APPLICANT: Perera, J. Ranjan
APPLICANT: Eagleton, Clare
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
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APPLICANT: Rice, Douglas A.
APPLICANT: Rice, Constitutive Maize Promoters
TITLE OF INVENTION: Constitutive Maize Promoters
FILE REFERENCE: 5718-33, 035718/175218
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                                                                                                                                     FILE REFERENCE: 11000.1036C2
CURRENT APPLICATION NUMBER: US/09/598,401C
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: U.S. NO. 6596925 60/146,591
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: PC/NZ00/00018
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: U.S. NO. 6596925 09/276,599
PRIOR FILING DATE: 1999-03-25
                                                                                                                                                                                                                                                                                                   APPLICANT: Eagleton, Clare
APPLICANT: Rice, Stephen J.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/257,584A
CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: 60/076,075
EARLIER FILING DATE: 1998-02-26
                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Zea mays
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25; Conserv
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Pred. No. 53;
0; Mismatches
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Pred. No. 53;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT ETLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-36
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SGO ID NOS: 207012
SOFTWARE: FAStSEQ for Windows Version 4.0
1.ENCTUL. 601
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 35388
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-35388
                                                                                  ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-35389
       Query Match 54.6%;
Best Local Similarity 75.8%;
Matches 25; Conservative
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US-09-949-016-35388
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35389, Application US/09949016 Patent No. 6812339
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR EILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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Best Local
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78.1%;
     Score 20.2; D
Pred. No. 85;
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Pred. No. 85;
0; Mismatches
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Pred. No. 64;
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

1. FULL OF THE COMMENT OF THE COMMENT OF SEQ ID NO 44448

T.FMCTUL. 601
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US-09-949-016-44447
; Sequence 44447, Appl
; Sequence 6812339
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                                                                                                                             Query Match
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                                                                                                                                                                                  LENGTH: 601
TYPE: DNA
ORGANISM: Human
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID 0 44447
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Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-09-08

PRIOR PRIOR PILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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TYPE: DNA
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25; Conservative
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GCATGGATTCCTGTGTTTGAAAGAAGCTTATAT 150
                               GCATGGAATTCTGGGCTTGAAAAAGGCTTGTTT 33
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75.8%;
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75.8%;
                                                                            Score 20.2; DI
Pred. No. 85;
0; Mismatches
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Pred. No. 85;
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OF DETECTION AND USES THEREOF
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US-09-533-559-5172/c

Sequence 5172, Application US/09533559 Patent No. 6902887

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LENGTH: 50810
TYPE: DNA
ORGANISM: Human
US-09-949-016-16039
RESULT 15
US-09-949-016-12642
; Sequence 12642, Application US/09949016
; Patent No. 6812339
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; ORGANISM: Aspergillus oryzae
US-09-533-559-5172
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US-09-949-016-16039/c
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PRILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R.Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjarke Olsen
                                                                                                                                                                                                           Best Loc
Matches
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Best Local Similarity
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LENGTH: 679
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                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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                                                                                                                            26480 AGGGAATTTTGGGCTTGAAGAAGGC 26456
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75.8%;
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Pred. No. 2.1e+02;
0; Mismatches 3;
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Pred. No. 87;
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                                                                                                                                                            ; ORGANISM: Human
US-09-949-016-12642
                                              Query Match
Best Local Similarity /5...
Thes 25; Conservative
                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12642
LENGTH: 54452
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/241,755
PRIOR TILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                    TYPE: DNA
43064 GCATGGATTCCTGTGTTTGAAAGAAGCTTATAT 43096
                       1 GCATGGAATTCTGGGCTTGAAAAAAGGCTTGTTT 33
                                                                                                 54.6%;
75.8%;
                                                                              0;
                                                                           Score 20:2; DB 3
Pred. No. 2.1e+02
0; Mismatches
                                                                                                                      DB 3;
                                                                                8
                                                                                                                    Length 54452;
                                                                                Indels
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Search completed: May 19, 2006, 02:34:32 Job time : 61.3542 secs THIS PAGE BLANK (USPTO)

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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                          seq
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           Published_Applications_NA_Main: *
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| EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd
1.0 37 3 US-09-211-691-5

1.0 37 7 US-10-317-478-5

1.0 37 7 US-10-317-478-5

1.0 16878 10 US-10-915-740A-62

1.4 2242716 10 US-10-750-185-19677

1.9 598 10 US-10-750-185-29101

1.9 795 10 US-10-750-185-29101

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1.9 136 8 US-10-437-963-88327

1.4 460 8 US-10-437-963-88327

1.4 460 7 US-10-027-632-34789

1.4 460 7 US-10-027-632-34789

1.5 6 US-10-027-632-34789

1.7 2613 13 US-11-097-143-25837

1.7 2613 13 US-10-027-172-243

1.8 560 4 US-09-925-065A-542557
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Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1068, Appl
Sequence 19677, A
Sequence 29101, A
Sequence 29101, A
Sequence 88295, A
Sequence 88297, A
Sequence 34789, A
Sequence 34789, A
Sequence 34789, A
Sequence 24837, A
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Sequence 34789, A
Sequence 34789, A
Sequence 24857,
Sequence 542557,
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US-10-301-480-629528	US-10-301-480-16119	US-10-450-763-4449	US-10-450-763-16289	US-10-425-115-39967	US-10-425-115-39969	US-10-425-114-35457	US-10-425-114-17871	US-10-425-115-3254	US-09-925-065A-156805	US-09-925-065A-156805	US-10-301-480-863413	US-10-301-480-250004	US-10-301-480-731611	US-10-301-480-731610	US-10-301-480-118202	US-10-301-480-118201	US-09-925-065A-16965	US-09-925-065A-16964	US-09-925-065A-16965	US-09-925-065A-16964	US-10-301-480-834789	US-10-301-480-221380	US-09-925-065A-123503	US-09-925-065A-123503	US-10-108-260A-841	US-10-017-161-1659	US-10-437-963-88306
Sequence 629528,	Sequence 16119, A	4449,	Sequence 16289, A	39967,	Sequence 39969, A	35457,	Sequence 17871, A	Sequence 3254, Ap	Sequence 156805,	Sequence 156805,	Sequence 863413,	Sequence 250004,	Sequence 731611,		Sequence 118202,	Sequence 118201,	16965,	Sequence 16964, A	Sequence 16965, A	Sequence 16964, A	Sequence 834789,	Sequence 221380,	Sequence 123503,	12350	Sequence 841, App	Sequence 1659, Ap	Sequence 88306, A

## ALIGNMENTS

```
APPLICANT: Gilbert, Michel
APPLICANT: Young, N. Martin
APPLICANT: Young, N. Martin
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
ITITLE OF INVENTION: Fusion Proteins for Use in En
ITITLE OF INVENTION: Oligosaccharides
FILE REFERENCE: 019957-012910US
FULL REFERENCE: 019957-012910US
CURRENT APPLICATION NUMBER: US/09/211,691
CURRENT FILING DATE: 1998-12-14
PROTOR APPLICATION NUMBER: US 60/069,443
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                                                                                                                                                                         US-09-211-691-5
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                                                                                  Query Match
Best Local S
Matches 37
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Patent No. US20020034805A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1997-12-15
                                                                                                                                                                                           FEATURE: OTHER INFORMATION: Description of Artificial Sequence:SIALM-22F OTHER INFORMATION: primer
                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                           37
                                                                                Similarity
                           GCATGGAATTCTGGGCTTGAAAAAGGCTTGTTTGACC 37
  GCATGGAATTCTGGGCTTGAAAAAGGCTTGTTTGACC 37
                                                                                  100.0%; Score 37; DB 3; llarity 100.0%; Pred. No. 4.3e-05; Conservative 0; Mismatches 0;
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RESULT 2 US-10-317-773-5 ; Sequence 5, Application US/10317773 ; Publication No. US20030180928A1

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RESULT 4
US-10-915-740A-62/c
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Young, N. Martin
APPLICANT: Young, N. Martin
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wational Research Council of Canada
ITITLE OF INVENTION: Nucleic Acid That Encodes a Fusion Protein
FILE REFERENCE: 019633-0000811US
CURRENT APPLICATION NUMBER: US/10/317,428
CURRENT FILING DATE: 2002-12-11
PRIOR APPLICATION NUMBER: US 60/069,443
PRIOR FILING DATE: 1997-12-15
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 09/211,691
PRIOR APPLICATION NUMBER: US 09/211,691
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
LENGTH: 37
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APPLICANT: Gilbert, Michel
APPLICANT: Young, N. Martin
APPLICANT: Young, N. Martin
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
ITILE OF INVENTION: GalNAc Transferase
ITILE OF INVENTION: GalNAc Transferase
FILE REFERENCE: 019633-000812US
CURRENT APPLICATION NUMBER: US/10/317,773
CURRENT FILING DATE: 2002-12-11
PRIOR APPLICATION NUMBER: US 60/069,443
PRIOR APPLICATION NUMBER: US 09/211,691
PRIOR PILING DATE: 1998-12-14
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                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:SIALM-22F; OTHER INFORMATION: primer US-10-317-428-5
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                                                                                                                                                                                        Matches
                                                                                                                                                                                                       Query Match
Best Local Similarity
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Publication No. US20030186414A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 37
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                              1 GCATGGAAITCIGGGCTTGAAAAAGGCTTGTTTGACC 37
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ilarity 100.0%;
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                                                                                                                                                                                                  Score 37; DB 7;
Pred. No. 4.3e-0
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APPLICANT: Mora, Manrosa
APPLICANT: Ratti, Giulio
APPLICANT: Scarselli, Maria
APPLICANT: Scarselli, Maria
APPLICANT: Scarlato, Vincenzo
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagratia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisseria Genomic Sequences And
FILE REFERENCE: 002441,00090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-915-740A-1068
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CURRENT FILING DATE: 2004-08-11
PRIOR APPLICATION NUMBER: 09/806,866
PRIOR FILING DATE: 1999-10-08
PRIOR PELLING DATE: 1998-10-09
PRIOR PELLING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: USSN 60/103,794
PRIOR APPLICATION NUMBER: USSN 60/132,068
PRIOR APPLICATION NUMBER: USSN 60/132,068
PRIOR APPLICATION NUMBER: PCT/US99/25373
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 1068
NUMBER OF SEQ ID NOS: 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Neisseria meningitidis US-10-915-740A-62
CURRENT APPLICATION NUMBER: US/10/915,740A
CURRENT FILING DATE: 2004-08-11
PRIOR APPLICATION NUMBER: 09/806,866
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: USSN 60/103,794
PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1068, Application US/10915740A
Publication No. US20050191316A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Pa
                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Frazer, Claire M.
APPLICANT: Hickey, Erin
APPLICANT: Peterson, Jeremy
APPLICANT: Tettelin, Herve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 62, Application US/10915740A Publication No. US20050191316A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Scarselli, Maria
APPLICANT: Scarlato, Vincenzo
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagratia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Their Use
FILE REFERENCE: 002441.00090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5806 TATGGGCTTGAAAAAGGCTTGTTTGACC 5779
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Masignani, Vega
Galeotti, Cesira
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Tettelin, Herve
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Masignani, Vega
Galeotti, Cesira
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                                                                                                                                            And Methods Of Their Use
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US-10-750-623-19677
; Sequence 19677, Application US/10750623
; Publication US20050287531A1
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; LENGTH: 2242716
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
; US-10-915-740A-1068
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SEQ ID NO 19677
LENGTH: 598
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILI100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
                                                             APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSERFELD, David
APPLICANT: HOLM, Tom
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SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 64922
                                             APPLICANT:
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LOCATION: (1)..(69)
OTHER INFORMATION: n is any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Bovine MMBT06634
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nes 27; Conserva
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CANT: BATES, Stephen
CANT: FANTIN, Dennis
OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
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HOLM, Tom
BATES, Stephen
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Pred. No. 12;
0; Mismatches
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Pred. No. 10;
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RESULT 9 US-10-750-623-29101

Sequence 29101, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard

APPLICANT: APPLICANT: APPLICANT:

> ROSENFELD, David HOLM, Tom BATES, Stephen

APPLICANT:

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APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION. COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMI1100-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 29101

LENGTH: 795

TYPE: DNA
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                                                                                                                                            ; TYPE: DNA
; ORGANISM: Bovine 19866880610988
US-10-750-185-29101
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 19677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29101, Application US/10750185 Publication No. US20050260603A1
                                                                                       Query Match
Best Local :
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Best Local (
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CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
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TYPE: DNA
ORGANISM: Bovine MMBT06634
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OTHER INFORMATION: n is any nucleotide
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                                                                                       Local Similarity
12 CATGGAATGCTGGGTTTGAGAAATGCTTGATTTA 45
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                                 2 CATGGAATTCTGGGCTTGAAAAAGGCTTGTTTGA 35
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                                                                        Conservative
                                                                                       65.9%;
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82.4%; Pred. No. 12;
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                                                                                       Score 24.4;
Pred. No. 13;
                                                                        Mismatches
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                                                                                                           DB 10;
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                                                                                                           Length 795;
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US-10-437-963-88327
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US-10-437-963-88295
/ Sequence 88295, Application US/10437963
/ Publication No. US20040123343A1
                                 APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Mu, Wei
APPLICANT: Boukharov, Andrey A
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_8715C.1 US-10-437-963-88295
                                                                                                                                                   Sequence 88327, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                 Matches
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SEQ ID NO 88295
LENGTH: 1386
                       TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(5221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEC. 1-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 29001
FENCEW: 25001
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APPLICANT:
APPLICANT:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS FILE REFERENCE: MMI1100-1 CURRENT APPLICATION NUMBER: US/10/750,623 CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
                  Cao, Yongwei

Wu, Wei

Boukharov, Andrey A.

Barbazuk, Brad

Li, Ping

Li, Ping
                                                                                                                                                                                                                                                                                      4 TGGAATTCTGGGCTTGAAAAAGGCTTGTTTGACC 37
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Zhou, Yihua
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Pred. No. 14
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Pred. No. 13;
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                                           RESULT 13
US-10-027-632-34789
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                                                                                                                                                    OTHER INFORMATION: n = A,T,C or US-10-027-632-34789
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
DETION DATE: 2000-03-29
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_8718C.
US-10-437-963-88327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-027-632-34789
                                                                               Matches
                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34789, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
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SEQ ID NO 88327
LENGTH: 1752
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(460)
                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                          LENGTH: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
       44
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                                          N
                                                                             26;
                                                                                         Similarity
CATGGAATCCTTGGCTAGAAAAAGGCTTG
                               CATGGAATTCTGGGCTTGAAAAAGGCTTG 30
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28; Conserv
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                                                                                         Score 24.2;
Pred. No. 14;
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Pred. No. 15;
                                                                    Mismatches
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                                                                                                     Length 460;
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Sequence 34789, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:

APPLICANT: Wang,

David G.

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PRIOR FILING DATE: 2000-04-20
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PELICATION NUMBER: US 60/185,218
PRIOR PELING DATE: 1900-02-24
PRIOR PELICATION NUMBER: US 60/167,363
PRIOR PELICATION NUMBER: US 60/156,358
PRIOR PELICATION NUMBER: US 60/156,358
PRIOR PELICATION NUMBER: US 60/16,358
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 460
TYPE: DNA
ORGANISM: Human
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25837, Application US/11097143 Publication No. US20050208558A1 GENERAL INFORMATION:
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APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
                                                 PRIOR APPLICATION NUMBER: 60/191,637 PRIOR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
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CURRENT EILING DATE: 2002-04-30
CRICA APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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                           NUMBER OF SEQ ID NOS: 43008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(460)
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                                                                                                  FILING DATE: 2000-01-12
APPLICATION NUMBER: 60/184,831
FILING DATE: 2000-02-24
                                                                                                                                                                                                     FILING DATE: 1999-11-12
APPLICATION NUMBER: 60/173,383
FILING DATE: 1999-12-28
                                                                                                                                                                               APPLICATION NUMBER: 60/175,693
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FastSEQ for Windows Version 4.0
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Pred. No. 1
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Search completed: May 19, 2006, 05:02:07

Job time : 641.094 secs

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; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-25837
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                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (208)..(1695)
US-10-302-172-243
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                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: pt_FL_genes
SEQ ID NO 243
LENGTH: 1734
                                                                                 Query Match
Best Local Similarity
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Best Local
                                                                 Matches
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TITLE OF INVENTION: No. US20040053250Alel Arginine-rich Protein-like Nucleic Acids
TITLE OF INVENTION: No. US20040053250Alel Arginine-rich Protein-like Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803_1CNCP
CURRENT APPLICATION NUMBER: US/10/302,172
CURRENT FILLING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/225,251
PRIOR FILING DATE: 2002-08-20
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT US02/05095
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/799,451
                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tang, Y. Tom
APPLICANT: Xue, Aidong J.
                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2613
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589 GAACTTCTGGGCTTTAAAAAGACTTGCTTGA 619
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28; Conserv
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                                                                 26;
                              5 GGAATTCTGGGCTTGAAAAAGGCTTGTTTGA 35
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                                                                 Conservative
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                                                                                 Score 23;
Pred. No.
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Pred. No. 51;
                                                               Mismatches
                                                                                     57;
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                                                                                                 Length 1734;
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Minimum
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Maximum Match 100%
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                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB
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seq length: 2000000000
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183.064 Million cell updates/sec
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                 Listing first 45 summaries
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           699
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                    00011111111110101011
     US-11-217-529-5602
US-10-505-928-46
US-10-528-032-8
US-10-528-032-8
US-11-217-529-2683
US-11-217-529-4718
US-10-515-937-470
US-11-217-529-2801
US-11-217-529-2801
US-11-217-529-1739
US-11-217-529-1739
US-11-217-529-76850
US-11-217-529-5552
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Sequence 10, Appl
Sequence 2683, Appl
Sequence 173201,
Sequence 4118, Ap
Sequence 470, Appl
Sequence 2801, Apple Sequence 2801, Apple Sequence 4580, Apple Sequ
Sequence 12, Appl
Sequence 23, Appl
Sequence 1739, Ap
Sequence 4700, Ap
Sequence 76150, A
Sequence 70850, A
Sequence 7023, A
Sequence 80619, A
Sequence 4421, Ap
Sequence 2011, Ap
Sequence 2011, Ap
Sequence 2955, Ap
Sequence 2552, Ap
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Sequence 546, App
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence						
191008,	190944,	190913,	190899,	191127,	190890,	190821,	3271, Ap	1053, Ap	173303,	4515, Ap	81626, A	5651, Ap	2017, Ap	77057, A	80280, A	1345, Ap	173771,	78791, A	2085, Ap

### ALIGNMENTS

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Sequence 5, Application US/11327900

Publication No. US20060099174A1

GENERAL INFORMATION:

APPLICANT: PHARMA PACIFIC

APPLICANT: Dran, Michel

APPLICANT: Tovey, Michael Gerard

TITLE OF INVENTION: INTERFERON-ALPHA INDUCED GENE

FILE REFERENCE: 4658/250044

CURRENT APPLICATION NUMBER: US/11/327,900

CURRENT APPLICATION NUMBER: US/10/203,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5602, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: SHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GEN
FILE REFERENCE: S-38-285
CURRENT FILING DATE: 2005-09-02
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR APPLICATION DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PATENTINI VERSION 3.3
SOFTWARE: PATENTINI VERSION 3.3
SEQ ID NO 5602
LENGTH: 699
TYDE: DNA
                                                                                                                                                                                                                                                                     RESULT 2
US-11-327-900-5
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Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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Conservative
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Pred. No.
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Sequence 546, Application US/10505928

Publication No. US20060088532A1

GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
ITILE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR FILING DATE: 2002-03-07

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866

SOFTWARE: Patentin 3.2

SEQ ID NO 546

LENGTH: 1904
US-10-528-032-8

JSEQUENCE 8, Application US/10528032

Publication No. US20060101530A1

GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.

TITLE OF INVENTION: RORS AS MODIFIERS OF THE P21 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX03-068C-US
CURRENT APPLICATION NUMBER: US/10/528,032

CURRENT APPLICATION NUMBER: US/10/528,032

CURRENT FILING DATE: 2005-03-16
PRIOR APPLICATION UMBER: US 60/411,010

PRIOR FILING DATE: 2002-09-16

PRIOR FILING DATE: 2002-09-16

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn version 3.2
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; ORGANISM: Homo sapiens
US-10-505-928-546
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US-10-505-928-546
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PRIOR APPLICATION NUMBER: GB 0002979.3
PRIOR FILING DATE: 2000-02-09
PRIOR PELING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: GB 0002982.7
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: GB 0002981.9
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
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Best Local 9
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Best Local Similarity
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NAME/KEY: CDS
LOCATION: (1)...(3705)
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TYPE: DNA
ORGANISM: Homo sapiens
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26; Conservative
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Pred. No. 9.4;
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8 ATTCTGGGCTTGAAAAAGGCTTGTT 32

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CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 2683
LENGTH: 882
                                                                            ; ORGANISM: Saccharomyces pastorianus US-11-217-529-2683
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US-10-528-032-10
; Sequence 10, Application US/10528032
; Publication No. US20060101530A1
; GENERAL INFORMATION:
                Matches
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-528-032-8
                             Query Match
Best Local :
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TITLE OF INVENTION: RORS AS MODIFIERS OF THE p21 PATHWAY AND METHODS OF USE FILE REFERENCE: EXG3-068C-USE CURRENT APPLICATION NUMBER: US/10/528,032 CURRENT FILING DATE: 2005-03-16 PRIOR APPLICATION NUMBER: US 60/411,010 PRIOR APPLICATION NUMBER: US 60/411,010 PRIOR FILING DATE: 2002-09-16 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin version 3.2

SEQ ID NO 10

LENGTH: 3586
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2683, Application US/11217529
Publication No. US20060099612A1
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Best Local :
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YUKIKO
APPLICANT: NAKAWURA, NOTKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJINURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
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Best Local Similarity
Matches 23; Conserv
                                                                                                                   TYPE: DNA
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                           Similarity
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         Conservative
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                        50.3%; Score 18.6;
84.0%; Pred. No. 16;
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Pred. No. 1
     Mismatches
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                                     Length 882;
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US-11-217-529-173201
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  밁
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SEQ ID NO 173201
LENGTH: 2154
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APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORTHISA
APPLICANT: KODAMA, YUKIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 173201, Application US/11217529 Publication No. US20060099612A1
                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.3 SEQ ID NO 4118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4118, Application US/11217529 Publication No. US20060099612A1
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Best Local Similarity
                                                                          Matches
                                                                                                                Query Match
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SUNTORY LIMITED APPLICANT: NAKAO, YOSHIHIRO APPLICANT: NAKAMURA, NORIHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
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                                                                                                                                                                                          TYPE: DNA
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                                                                                            Local
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ATGAATTTTTCGCCTTCCAAAAGGATTCTTTGA 895
                                    ATGGAATTCTGGGCTTGAAAAAGGCTTGTTTGA 35
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KODAMA, YUKIKO
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Pred. No. 21;
0; Mismatches
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Pred. No. 21
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RESULT 9

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APPLICANT: ASHKKAI; TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT FAPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2801
LENGTH: 2868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2801, Application US/11217529 Publication No. US20060099612A1 GENERAL INFORMATION:
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SEQ ID NO 470
LENGTH: 2781
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Best Local
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PRIOR PILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR PILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE REFERENCE: 506612000104
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511, 937
CURRENT FILING DATE: 2004-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKANURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
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  684 GGAATCCTTGATCTGAAAAAAGCTCGTATTACC 652
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                                      5 GGAATTCTGGGCTTGAAAAAGGCTTGTTTGACC 37
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Prentice, James
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Pred. No. 22;
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RESULT 11

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CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 4580
LENGTH: 1689
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Publication No. US20060088532A1

GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
LENGTH: 3856
TYUEN DATE: 3856
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                                                                                                                               US-11-246-999-12/c
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US-11-217-529-4580
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US-11-217-529-4580/c
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                     Sequence 12, Application US/11246999
Publication No. US20060099622A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PF489P2
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APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUUKKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHHIK
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Best Local
CURRENT APPLICATION NUMBER: US/11/246,999
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Publication No. US20060099612A1
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APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                               690 ATCGAAATCGTCGATTGACAAGGGCTTGTTT 660
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KODAMA, YUKIKO
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Pred. No. 28;
0; Mismatches
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Pred. No. 24;
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FILE REFERENCE: PF469P2

CURRENT FILING DATE: 2005-10-11

PRIOR APPLICATION NUMBER: US/11/246,999

CURRENT FILING DATE: 2005-10-11

PRIOR APPLICATION NUMBER: US/09/984,130

PRIOR FILING DATE: 2001-10-29

PRIOR PFLICATION NUMBER: 09/243,792

PRIOR PFLICATION NUMBER: 09/836,353

PRIOR PFLICATION NUMBER: 09/836,353

PRIOR APPLICATION NUMBER: 00/198,407

PRIOR APPLICATION NUMBER: 60/198,407

PRIOR PILING DATE: 2000-04-19

PRIOR PILING DATE: 1909-10-27

PRIOR PILING DATE: 1999-10-27

PRIOR APPLICATION NUMBER: 60/105,971

PRIOR PILING DATE: 1998-10-28

NUMBER: OF SRO ID NOS: 149
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                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-246-999-23
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SEQ ID NO 12
LENGTH: 2499
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2005-10-11
PRIOR APPLICATION NUMBER: US/09/984,130
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR APPLICATION NUMBER: 09/836,353
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: 60/198,797
PRIOR APPLICATION NUMBER: 60/198,797
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 149
                                                                                                                                                                                                                              SOFTWARE: P.
                                                                                              Query Match
Best Local
                                                                                  Matches
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TITLE OF INVENTION: 12 Human Secreted Proteins
                                                                                                                                                                                                             ENGTH:
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es 23; Conserv
2133 TGGCATTTGGGGCTGGATAATTCCTTGTTTG
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23; Conservative
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                            TGGAATTCTGGGCTTGAAAAAGGCTTGTTTG 34
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Pred. No. 31;
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2103
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RESULT 15 US-11-217-529-1739/c ; Sequence 1739, Application US/11217529 ; Publication No. US20060099612A1

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GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED

APPLICANT: NACAGO, YOSHIHIRO

APPLICANT: NACAGO, YOSHIHIRO

APPLICANT: NACAGOA, WINIKO

APPLICANT: NACAGOA, WINIKO

APPLICANT: KODAMA, WINIKO

APPLICANT: KODAMA, WINIKO

APPLICANT: ASHIKARI, TOMOKO

APPLICANT: ASHIKARI, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIRO

ITITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILLE REFERENCE: S-38-285

FILE REFERENCE: S-38-285

CURRENT FILING DATE: 2005-09-02

PRIOR APPLICATION NUMBER: US/11/217,529

CURRENT APPLICATION NUMBER: US 10/932,182

PRIOR FILING DATE: 2004-09-02

PRIOR APPLICATION VERSION 3.3

SOPTWARE: PATCHIN version 3.3

SOPTWARE: PATCHIN version 3.3

SEQ ID NO 1739

LENGTH: 2565

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-11-217-529-1739

Query Match

Best Local Similarity 74.2%; Score 18.2; DB 7; Length 2565;

Best Local Similarity 74.2%; Pred. No. 32;

Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps

Oy

S GGAATTCTGGGGTTTAAAAATGTGTTTTGA 35

Db 1007 GTAATACTGGGGTTTAAAATGTGTTTTTGA 977

Search completed: May 19, 2006, 04:25:03

Job time: 14.2604 secs
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description
ן	37.4	63.4	63	2	AR105314	AR105314 Sequence
N	37.4	63.4	63	N	AR144761	
ω		63.4	63	N	BD009737	_
4		60.7	60	N	BD134501	BD134501 Lipopolys
ហ		60.7	60	N	AR473909	AR473909 Sequence
6		60.7	60	N	AR489132	
		59.7	1149	N	AR393465	AR393465 Sequence
		59.7	1542	N	AR393466	
		59.7	1569	N	AR224042	
	•	59.7	1728	N	AR393467	AR393467 Sequence
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	٠	57.3	530	8	AJ619720	AJ619720 Expressio
		57.3	530	æ	AJ619721	AJ619721 Expressio
c 17	•	57.3	867	N	AR139130	AR139130 Sequence
18	33.8	57.3	867	N	AR139131	AR139131 Sequence

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ALIGNMENTS	CS086371 BD096937 BD206135 AX011208	AX717008 AX717008 AX404871 AX777477 AX404869	AX512658 ASY14585 SCFV1858290 DD196882 AC122106	A83226 BD096923 BD096924 AR182950 AR182951 AX472008	AR139128 AR139129 AX642595 AX642592 AR82175 CVE243206 CVE243206 AJ617284 A83225
	CS086371 Sequence BD096937 Mutated O BD206135 Polyvalen AX011208 Sequence	Sequence Sequence Sequence Sequence	<b>~</b> ~ ~	A83226 Sequence 46 BD096923 Chemical BD096924 Chemical AR1B2950 Sequence AR1B2951 Sequence AX477008 Sequence	AR139128 Sequence AR139129 Sequence AX642595 Sequence AX642592 Sequence A82175 Sequence 10 AJ243206 Cloning v AJ617284 Synthetic A83225 Sequence 45

KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 2 AR144761 LOCUS DEFINITION ACCESSION VERSION	Qy dd	Query Match Best Local   Matches 4	SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE ORIGIN	RESULT 1 AR105314 LOCUS DEFINITION ACCESSION VERSION VERSION
, 1 ed	AR144761 63 bp DNA 1 Sequence 8 from patent US 6210933. AR144761 AR144761 GI:15106628	1 CCTAGGTCGACTCATTAGTGGTGATGGTGGTGATGGTTCAGGTCTTC	63.4%; Score 37.4; DB 2; Similarity 87.2%; Pred. No. 0.0011; 1; Conservative 0; Mismatches 6;	Unknown. Unknown. Unclassified. 1 (bases 1 to 63) 1 (bases 1 to 63) Gilbert,M., Wakarchuk,W.W., Young,M.N. and Gilbert,M., Wakarchuk,Jsialyltransferases a Patent: US 6096529-A 8 01-AUG-2000; Location/Qualifiers 1. 63 /organism="unknown" /mol_type="unassigned DNA"	AR105314 63 bp DNA 1 Sequence 8 from patent US 6096529. AR105314 GI:12818911
, Jenning	linear	GTCTTC 47	Length 63; Indels	Jennings,M.P. and their use	linear
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Recombinant alpha-2,3-sialyltransferases and their uses
L Patent: JP 2001503961-A 6 27-MAR-2001;
NATIONAL RESEARCH COUNCIL OF CANADA
OS Unidentified
PN JP 2001503961-A/6
PD 27-MAR-2001
PF 10-JUN-1997 JP 1997526320
PF 10-JUN-1997 JP 1997526320
PF 0-JUN-1997 JP 1997526320
PC C12N1S/54,C12N15/70,C12N15/79,C12N9/10,C12N5/10,C12N1/:
C12P19/26
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source

1..63
/organism='Unidentified'.
                   BD134501 60 b

Lipopolysaccharide alpha-2,3 s

jejuni and its uses.

BD134501 GI:23229446

JP 2002507424 A/3.
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Recombinant alpha. -2,3-sialyltransferases and Patent: US 6210933-A 8 03-ApR-2001;

Location/Qualifiers
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JP 2001503961-A/6.
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19/26
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construct
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/mol_type="unassigned DNA"
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Patent: JP 2002507424-A 3 12-MAR-2002;
NATTONAL RESEARCH COUNCIL OF CANADA
OS Artificial Sequence
PN JP 2002507424-A/3
PD 12-MAR-2002
PF 22-MAR-1999 US 60/078891.18-MAP-1
PR 20-MAR-1998 US 60/078891.18-MAP-1
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1 (bases 1 to 60)

Gilbert, M. and Wakarchuk, W.W.
Lipopolysaccharide .alpha.-2,3 sialyltransferase
jejuni and its uses
Patent: US 6689604-A 4 10-FEB-2004;
...innal Research Council of Canada; Ottawa;
AR489132
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PD 12-MAR-2007
PD 12-MAR-2008
PF 22-MAR-1999 JP 2000538012
PR 20-MAR-1998 US 60/078891,18-MAR-1999
PR 20-MAR-1998 US 60/078891
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1 (bases 1 to 60)
Gilbert,M. and Wakarchuk,W.W.
Lipopolysaccharide alpha-2,3 sialyltra
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Wood,K.W., Finer,J.T., Beraud,C., Mak,J. and Sakowicz,R.
Methods of screening for modulators of cell proliferatio
Patent: US 6617115-A 3 09-SEP-2003;
Cytokinetics, Inc.; South San Francisco, CA
Location/Qualifiers
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Sequence 3 from
AR393465
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Gilbert, M. and Wakarchuk, W.W.
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1 (bases 1 to 1542)
Wood,K.W., Finer,J.T., Beraud,C., Mak,J. and
Wethods of screening for modulators of cell p
Patent: US 6617115-A 5 09-SEP-2003;
Cytokinetics, Inc.; South San Francisco, CA
Location/Qualifiers
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/mol_type="genomic
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/mol_type="genomic DNA"
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Wood,K.W., Finer,J.T., Beraud,C., Mak,J. and Sakowicz,R.
Methods of screening for modulators of cell proliferatic
Patent: US 6617115-A 7 09-SEP-2003;
Cytokinetics, Inc., South San Francisco, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1569)
Beraud, C., Finer, J.T., Sakowicz, R. and Wood, R
Methods of identifying modulators of kinesin
Patent: US 6440684-A 3 27-AUG-2002;
Cytokinetics, Inc., South San Francisco, CA
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/mol_type="genomic
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                                             Synthetic mRNA sequence for human alpha-1,3-galactosyltransferase.
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               alpha-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (14-MAR-1997) N.O.L.
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human blood group A glycosyltransferase;
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       1 GI:1041669
,3-galactosyltransferase;
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LTPCRKDVLVVTPMLAPIVMEGTENIDILNEQFRLQNTTIGLTVFAIKKYVAFLKLFL
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SQAYLPKDBGDFYLLGGFFGGSVQEVQRLTRACHQAMMVDQANGIEAVWHDESHLNK
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                                                                                                                                                                                                                                                        /gene="ompA"
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/protein_id="CAA72635.1"

/db_xref="G1:1903017"
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/note="soluble enzyme"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="synthetic construct"

mol_type="other RNA"

db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="ompA"
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68
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                                                                                                                                                                                                          59.0%;
94.7%;
                                                                                                                                                                                          Score 34.8; DB 8;
Pred. No. 0.0078;
0; Mismatches 2;
                                                                         1034 bp
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human blood group A
    synthetic gene
                                                            plood
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                                                         group B
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Zhang,J.
Direct Submission
Direct Submission
Submitted (16-DEC-2003) Zhang J., Institute for Biological
Sciences, National Research Council, 100 Sussex Dr., Ottawa,
Ontario, K1A 086, CANADA
                                                                                                                                                                                                      Zhang, J. and MacKenzie, R. Plasmid vectors for the construction
                                                                                                                                                                                                                                                                AJ619718.1 GI:41411187

pentavalent protein 1.

Expression vector pVT1

Expression vector pVT1

other sequences; artificial sequences; vectors.
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Overlaps with J05175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGATGGTGGTGATGGTTCAGGTCTTCTTCGCTGATCAG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seto,N.O., Palcic,M.M., Hindsgaul,O., Bundle,D.R. and Narang,S.A. Expression of a recombinant human glycosyltransferase from a synthetic gene and its utilization for synthesis of the human blood group B trisaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGTGATGGTGATGGTTCAGGTCTTCTTCGCTGATCAG 981
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LTPCKKUVLVTPMLAPIVMEGTENIDILNEQFKLQNTTIGLTVPAIKKYVAFLKLFL
STAEKHEMVGHRVHXVVFTDQPAAVPRVTLGTGRQLSVLEVGAXKRVQDVSMRRMEMI
SDFCERRFLSSVDXLVVVFTDQPAAVPRVTLGTGRQLSVLEVGAXKRVQDVSMRRMEMI
SQAXIFKDBGDFYYMGAFFGGSVQEVQRLTRACHQAMMVDQANGIEAVMHDESHLNK
YLLRHKPTKVLSPEYLMDQQLLGMPAVLRKLRFTAVPKNHQAVRNPEQKLISEEDLNH
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/db xref="taxon:32630"
/note="synthetic human cDNA with E.coli preferred codons
and E.coli insert"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="blood group B alpha-1,3-galactosyltransferase"
/protein id="CAA62976.1"
/db_xref="GI:1041670"
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                        Submitted (16-DEC-2003) Zhang J., Institute for Sciences, National Research Council, 100 Sussex Ontario, K1A 0R6, CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  pentavalent protein 2.
Expression vector pVT2
Expression vector pVT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ619719.1 GI:414111189
pentavalent protein 2.
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Expression vector pVT2 synthetic
                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                      other sequences; artificial
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               /translation="MKKTAIAIAVALAGFATVAQAVFVRSGFGGGSGGGGSTPDCVTG
KVEYTKYNDEDTFTVKVGDKELFTNRANLQSLLLSAQITGMTVTIKTNACHNGGGFSE
VIFRGGGGSGLAGSEQKLISEEDLNHHHHH"
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KVEYTKYNDDDTFTVKVGDKELFTNRWNLQSLLLSAQITGMTVTIKTNACHNGGGFSE
VIFRGGGGSGLAGSEQKLISEEDLNHHHHH"
                                                                                                                                                                                    /organism="Expression v
/mol_type="other DNA"
/db_xref="taxon:262221"
                                                          /product="pentavalent protein 2 precursor"
/protein_id="CAF22054.1"
/db_xref="GI:41411190"
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/experiment="experimental evidence, no add
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recorded"
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recorded"
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|mol_type="other DNA"
|db_xref="taxon:262220"
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/protein_id="CAF22053.1"
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/transl_table=11
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gene for pentavalent protein 2
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Expression vector pVT3
other sequences
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AJ619720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-DEC-2003) Zhang J., Institute for Sciences, National Research Council, 100 Sussex
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Plasmid vectors for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang, J
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                         TTAGTGGTGATGGTGATGGTTCAGGTCTTCTTCGCTGATCAG 59
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                                                                                                                                                                                                                                                      /codon_start=1
/transI_table=11
/transI_table=11
/product="pentavalent protein 3 precursor"
/protein_id="CAP22055,1"
/protein_id="CAP22055,1"
/db_xcef="GI:41411192"
/translation="MKKTAIAIAVALAGFATVAQAVFVRSGPGGGSGGGGSTPDCVTG
/translation="MKKTAIAIAVALAGFATVAQAVFVRSGPGGGSGGGGSTPDCVTG
KVEYTKYNDDDTFTVKVGDKELATNBANLQSLLLSAQITGMTVTIKTNACHNGGGFSE
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/experiment="experimental eviden
recorded"
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/experiment="experimental evidence, no add
recorded"
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recorded"
                                                                                                                                                                                                               experiment="experimental evidence,
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                                                                                                                                                                                                                                                                                                                                                                            /experiment="experimental
                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Expression vector
|mol_type="other DNA"
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84.4%;
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Search completed: May 19, 2006, 01:27:34 Job time : 1259.67 secs

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59
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	59.7	59.7	59.7	59.7	60.7	63.4	100.0	Match	Ouerv	۴
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ACA62168	AAD04538	AAD04537	AAV10118	ABK97798	ADO52298	ADO52300	ACA62170	AAD04540	AAD04539	AAV10119	AAC85783	ABS55161	AAC85782	AAC85781	AAZ25695	AAV04130	AAX84285	ID		
Aca62168 C-antigen	Aad04538 Human H11	Aad04537 Human mon	Aav10118 Human H11	Abk97798 C219scFv	Ado52298 Human ant	Ado52300 Human ant	Aca62170 C-antigen	Aad04540 Human Hll	Aad04539 Human mon	Aav10119 Human Hll	Aac85783 cDNA enco	Abs55161 Human HsK	Aac85782 cDNA enco	Aac85781 cDNA enco	Aaz25695 Campyloba	Aav04130 Neisseria	Aax84285 PCR prime	Description		

This sequence represents a PCR primer for the Neisseria alpha-2,3-sialyltransferase coding sequence. The invention relates to a nucleic acid encoding a fusion protein that comprises a glycosyltransferase

A new glycosyltransferase fusion protein useful in the enzymatic synthesis of oligosaccharides.

Example 1; Page 40; 63pp; English.

WPI; 1999-395174/33.

Gilbert M,

Wakarchuk WW;

(CANA ) NAT RES COUNCIL CANADA. Young NM,

C 45	44										C 34								c 26			c 23			20	c 19
27.4	28	28.4	28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	29	29	29	29	29	29.2	31.2	32.2	33	33	33.6	33.8	33.8	33.8	33.8
46.4	47.5	48.1	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	49.2	49.2	49.2	49.2	49.2	49.5	52.9	54.6	55.9	55.9	56.9	57.3	57.3	57.3	57.3
72	70	1574	4570	1897	1817	1817	1794	1698	1653	898	888	1977	1906	1806	1806	705	3093	88	2013	72	72	206	3604	1152	918	918
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AAZ21147	AEG11345	AAZ57599	AAF61152	ADE29201	ACC79607	ACC79606	AAV73337	AAZ43431	AAZ43432	AAV73335	ADZ66383	ABA99913	ADD13791	ABL61057	ABA99914	ADB85116	ADD14876	ABN84817	ABL59152	AAV72071	AAV72070	AAV81221	ABK97805	ABK97808	AD052297	AD052295
Aaz21147 C-myc pep	Aeg11345 P. falcip	Aaz57599 Erythrocy	Aaf61152 Single ch	Ade29201 Multivale	Acc79607 Plasmid p	Acc79606 Plasmid p				Aav73335 Mouse OKT	Adz66383 MOF11 ant	Aba99913 TNF-selec	Add13791 Plasmid p	Abl61057 TNF-selec	Aba99914 TNF-selec	Adb85116 TNF fusio	Add14876 Phage dis	Abn84817 Human DNa	Abl59152 Sequence		Aav72070 806.077 s	Aav81221 Plasmid p	Abk97805 Interfero	Abk97808 DNA encod	7	

## ALIGNMENTS

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RESULT 1
AAXA8428
IID AAXA8
XX AAXA8
XX AAXA8
XX Beta
XX Beta
XX Beta
XX Garb

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Neisseria sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1997;
14-DEC-1998;
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98US-00211691.
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Length

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RESULT 2
AAV04130
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Matches 59
          AAV01427-V01430 are PCR primers used in the amplification of novel alpha-2,3-sialyltransferase from Neisseria meningitidis and Neisseria gonorrheae. The protein can be used as a resgent for adding a sialic acid residue to an acceptor having a terminal galactose residue, e.g. in synthesis of biologically active oligosaccharides or sialyl-modified proteins or lipids. The nucleic acid sequence can be used for the recombinant production of alpha-2,3-sialyltransferase
                                                                                                                                                                               Nucleic acid sequence encoding Neisseria alpha-2,3-sialyl:transferase useful to add sialic acid to acceptor with terminal galactose residue synthesis of biologically active oligosaccharide.
                                                                                                                                                   Example 2; Page 25; 50pp; English
                                                                                                                                                                                                                                                              WPI; 1998-052313/05.
                                                                                                                                                                                                                                                                                               Gilbert M,
                                                                                                                                                                                                                                                                                                                                                             10-JUN-1996;
07-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catalytic domain and a catalytic domain from an accessory enzyme that is involved in formation of a nucleotide sugar which is a saccharide donor for a glycosyltransferase reaction. The fusion protein is useful in the catalyse more than one reaction involved in the fusion proteins are able to is useful for the development of therapeutic agents that have specific carbohydrate structures. Carbohydrates are involved in recognition such the surface of cells. The fusion protein can be used for the synthesis of the synthesis of the synthesis of both natural carbohydrates and synthetic derivatives with reactions in a single vessel, provides improved yields of end products. Teduced. The fusion protein can be used for the source of the synthesis of the surface of cells. The fusion synthetic derivatives with reactions in a single vessel, provides improved yields of end products is reduced. The fusion protein can also use directly different donor analyses and various and various and various arith a transital loss.
                                                                                                                                                                                                                                                                                                                                 (CANA ) NAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha-2,3-sialyltransferase; sialic acid; acceptor; lipid; PCR primer; biologically active oligosaccharide; sialyl-modified protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV04130 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV04130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCTAGGTCGACTCATTAGTGGTGATGGTGATGGTTCAGGTCTTCTTCGCTGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                             Wakarchuk
                                                                                                                                                                                                                                                                                                                                 RES
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97US-00872485
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                                                                                                                                                                                                                                                                                          Young NM,
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Pred. No.
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AAC85781 standard;

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                                                                                                                                                                                         The present sequence represents a PCR primer for the Campylobacter jejuni cst-I gene which encodes alpha-2,3-sialyltransferase. The alpha-2,3-sialyltransferase protein is useful for producing desired carbobydrate structures by contacting the acceptor molecule (which has a terminal galactose residue) with an activated sialic acid molecule. The terminal galactose residue is linked to a second residue (Glc or a GlcNac, or GlcNac or GalNac) in the acceptor molecule through a beta-1,3 or beta-1,4 linkage, respectively. The activated sialic acid is CMP-Neu5Ac. The polynucleotides and polypeptides facilitate the improved production of desired structures and nucleic acids encoding sialyltransferases
                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                       New sialyltransferases useful for adding sialyl residues to acceptor
                                                                                                                                                                                                                                                                                                                                                                                                            Gilbert M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1998;
18-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campylobacter jejuni; alpha-2,3-sialyltransfarase; lipopolysaccharide; galactose residue; sialic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campylobacter jejuni alpha-2,3-sialyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ25695;
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                                                                                  μ.
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                                                                                                                               40;
                                                                                                                                       Similarity
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                                                                                             CCTAGGTCGACTCATTAGTGGTGATGGTGGTGATGGTTCAGGTCTTC
                                                                         CCTAGGTCGACTCATTAGTGGTGATGGTGATGTTCCCCCTTTCTC
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                                                                                                                                                                          BP; 9
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                         Page 14; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            Wakarchuk
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99US-00272960.
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                                                                                                                                                                        A; 17 C; 13 G;
                                                                                                                                      60.7%;
85.1%;
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87.2%;
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                                                                                                                                      Score 35.8;
Pred. No. 0.
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); Mismatches
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Pred. No. 0.0094;
                                                                                                                        Mismatches
                                                                                                                                                                      21 T; 0 U; 0 Other;
                                                                                                                                  .031;
                                                                                                                                                 DB
                                                                                                                                                2
                                                                                                                        7;
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                                                                                                                                              Length 60;
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer
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molecule; PCR primer;
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RESULT 5
AAC85782;
ID AAC85782;
XX
AC AAC85782;
XX
DT 18-JUL-2001 (first entry)
XX
DE cDNA encoding KSP-K491.
XX
Human; kinesin; KSP; drug screen
XX
XX
Synthetic.
XX
PN W0200131335-A2.
XX
PF 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029570.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1149 BP; 367 A; 207 C; 269 G; 306 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression of KSP, where the cells are cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; kinesin;
ATP hydrolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding KSPL360
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DB; AAB47213.
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                                                                                                                                                                                                                                                                                                                TCAGTGGTGGTGGTGGTGCTCGATCAGGTCCTCCTCGCTGATCAG
                                                                                                                                                                                                                                                                                                                                 TCATTAGTGGTGATGGTGGTGATGGTTCAGGTCTTCTTCGCTGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finer JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for drug candidates and treating
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSP; drug screening; mitotic spindle; mitosis; apoptosis; necrosis; cancer; ss.
                                                                                                                KSP; drug screening; mitotic spindle; mitosis; apoptosis; necrosis; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; 63pp;
                                                                                                                                                                                                                                                                                                                                                                                       59.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beraud
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                                                                                                                                                                                                                                                                                                                                                                       Score 35.2; DB 4;
Pred. No. 0.087;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakowicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer by using kinesin KSP
                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                   Length 1149;
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RESULT 6
ABS551.61/c
ID ABS551
XX ABS551
XX ABS551
XX Human
XX Microt
KW Myperp
KW inflam
KW inflam
KW inflam
KW inflam
KW angiop
XX Homo s
OS Synthe
FT CDS
FT CDS
FT CDS
FT T misc_f
FT misc_f
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Microtubule stimulated ATPase; cellular proliferation; cancer; AIDS; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; HIV; inflammation; autoimmune disease; arthritis; graft rejection; psoriasis; inflammatory bowel disease; proliferation; medical procedure; surgery; human immunodeficiency virus; acquired immunodeficiency syndrome; angioplasty; human; HsKif4; kinesin family; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           candidate agents on apoptosis and necrosis. The method of the invention is useful for screening for drug candidates (especially bioactive agents and proteins) which effect the bioactivity of KSP, binding to KSP and/or
  US6440684-B1
                                                                                            misc_feature
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                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS55161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1542 BP; 528 A; 257 C; 354 G; 403 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression of KSP, where the cells are cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening for drug candidates and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-300550/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                 1549.
                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                 /note= "Encodes 6-histidine residues at C-terminus"
                                                                                                                       /note= "Encodes
                                                                                                                                         *tag=
                                                                                                                                                                  1486. .1548
                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                           'note= "Encodes
                                                                                                                                                                                                                                                           product= "Human HsKif4 construct protein"
                                                                                                                                                                                                                                                                                                             .1569
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83.3%;
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Pred. No. 0.
                                                                                                                                                                                           N-terminal T7 epitope
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                                                                                                                     C-terminal myc epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer by using kinesin KSP.
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AAC85783/c
ID AAC857
XX AAC857
AC AAC857
DT 18-JUL
XX CDNA e
XX Human;
KW Human;
KW ATP hy
XX Synthe
XX Synthe
XX WO2001
XX PD 03-MA)
XX ATP
PD 03-MA)
XX X PF 26-OC7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC The present invention relates to a new method of screening modulators of CC target protein with microtubule stimulated ATPase activity. The method CC involves contacting the target protein with an agent at 1st and 2nd CC concentrations and determining the level of activity (e.g. binding or CC ATPase activity) of target protein where a difference between levels of CC activity of target protein contacted with 1st and 2nd concentrations of CC an agent indicates that an agent modulates activity of target protein. CC having microtubule stimulated ATPase activity. The compounds identified CC including cancer, hyperplasias, restenosis, cardiac hypertrophy, immune CC disorders and inflammation. The compounds identified by the method are inflammatory bowel disease, proliferation induced by medical procedures, cc 9. surgery, angioplasty ecc. The compounds are also useful for treating autoimmune disease, arthritis, graft rejection, CC e.g. surgery, angioplasty ecc. The compounds are also useful for treating course (HIV) and thus treating acquired immunodeficiency syndrome (AIDS). CC The present nucleic acid sequence encodes the human HsKif4 (kinesin XXX)
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
        26-OCT-2000; 2000WO-US029570
                                               03-MAY-2001.
                                                                                                          Synthetic
                                                                                                                                    Human; kinesin; ATP hydrolysis;
                                                                           WO200131335-A2
                                                                                                                                                                                cDNA encoding
                                                                                                                                                                                                                18-JUL-2001
                                                                                                                                                                                                                                              AAC85783;
                                                                                                                                                                                                                                                                 AAC85783 standard; cDNA; 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1569 BP; 482 A; 331 C; 389 G; 367 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening for modulators of target protein having microtubule stimulated ATPase activity e.g. kinesin family of protein, useful for treating cancer, psoriasis, arthritis, human immunodeficiency virus (HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
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                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                KSP-S553
                                                                                                                            KSP; drug screening; mitotic spindle; mitosis; apoptosis; necrosis; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sakowicz
                                                                                                                                                                                                                                                                                                                                                                                                    Score 35.2; D
Pred. No. 0.09
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1569;
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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RESULT 8
AAV10119/c
ID AAV101:
XX AAV101:
XX 29-MAY.
XX 20-MAY.
XX Hull; mu
KW H11; mu
KW V regin
KW primer
KW malignn
KW single
XX Synther
OS Synther
OS Homo s:
XX FT CDS
FT CDS
FT CDS
FT T CDS
FT T TOS
XX PN WO9744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                       22-MAY-1996;
                                                                    22-MAY-1997;
                                                                                                                       27-NOV-1997
                                                                                                                                                                      WO9744461-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H11; monoclonal antibody; MAb; C-antigen; variable region heavy V region; H chain; neoplasia; detection; lymphoma; tumour cell; primer; vaccine; gene therapy; glioblastoma; neuroblastoma; malignant melanoma; adenocarcinoma; small cell lung carcinoma; single chain variable region; scFv; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human H11-scFv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV10119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV10119 standard; DNA; 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes the kinesin, KSP-S553, which may be used in the method of the invention to screen for drug candidates and bioactive agents. The method comprises combining the candidate and a cell expressing recombinant KSP, and determining the effect of the candidate on the bioactivity of recombinant KSP. Changes in the bioactivity of KSP may be determined by assays for determining changes in the mitotic spindle, particularly inhibition of mitosis, and ATP hydrolysis. It may candidate agents on apoptosis and necrosis. The method of the invention is useful for screening for drug candidates (especially bioactive agents and proteins) which effect the bioactivity of KSP, binding to KSP and/or expression of KSP, where the cells are cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1728 BP; 594 A; 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 7; 63pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening for drug candidates and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-300550/31.
P-PSDB; AAB47215.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CYTO-) CYTOKINETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1728
                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 TCATTAGTGGTGATGGTGGTGATGGTTCAGGTCTTCTTCGCTGATCAG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGTGGTGGTGGTGGTGCTCGATCAGGTCCTCCTCGCTGATCAG 1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Finer JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                     96US-00657449
                                                               97WO-US008962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     construct dimer forming DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encodes the kinesin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00428156
                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                           interrupted by an intron
856. .861
                                                                                                                                                                                                                                                                   /product= "H11-scFv construct"
/note= "partial sequence of di
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.7%;
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                                                                                                                                                                                                                                                                                                                                          D)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.2; DB Pred. No. 0.093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; 393 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mak J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               450 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sakowicz
                                                                                                                                                                                                                                                                                dimer forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
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RESULT 9
AAD04539/c
ID AAD045
XX
AC AAD045
XX
AC AAD045
XX
DE Human
XX
Human
XX
Human
XX
Homo s
XX
C-anti
XX
FT CDS
FT
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VX
US6207
XX
PR
22-MAY
XX
AAD045
AD045
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Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neoplastic disease; melanoma; immunoglobulin IgM; gene therapy; lymphoma; carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine; neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic; c-antigen; chronic leukaemia; glioma; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes a human H11 monoclonal antibody single chain V region fragment (H11-scFv) construct which is capable of forming dimers. This construct is used to determine the ability of H11-scFv antibody fragments to bind specifically to the C-antigen on cancer cells. Such antigen binding fragments may be used for treating a patient with neoplasia. It is especially useful in the detection of lymphomas and leukaemias where the tumour cells bearing the C antigen are circulating in the patients bloodstream. The polynuclectide sequence may be used as a primer or a probe and the encoded protein may be used in a vaccine or for gene therapy. The human monoclonal antibody (MAb), designated H11, specifically recognises cancerous cells. H11 is specific for glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma and monocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human monoclonal antibody H11-single chain variable region (scFv) DNA #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen binding fragment from monoclonal antibody, H11 - allows tumour specific detection and treatment of neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD04539 standard; DNA;
      22-MAY-1996;
                                                         22-MAY-1997;
                                                                                                                                                                          US6207153-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-018515/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCACTAATGGTGATGGTTCAGATCTTCTTCGCTGATCAG 817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
      96US-00657449
                                                                                                                                                                                                                                                                  reading frame; codons"
                                                                                                                                                                                                                                                                                          product= "Human H11-single chain variable region (scFv)" (trans1 except= (pos:853. .864, aa:His-Lys) (note= "Insertion of two inframe stop codon alters the reading frame; CDS does not include start and stop
                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33.8; DB Pred. No. 0.24; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; 241 G; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc single chain variable region (scFv). The Hill light chain variable region cc single chain variable region (scFv). The Hill light chain variable region through a (SGGGG) 3 linker to consider the heavy chain variable region through a (SGGGG) 3 linker to consider the first consideration relates to human monoclonal antibody (Mab) cc Hil, Hil-(scFv) single chain variable (V) region fragment and their corresponding DNA molecules. Hil antibody is an immunoglobulin of IgM could subclass which is specific to C-antigen found specifically on neoplastic cells and not on normal cells. Hil is an antibody obtained from the cells and not on normal cells. Hil is an antibody obtained from the compared ploma and fused to a human myeloma cell line to produce a chybridoma designated NBGM1/HIL A pharmaceutical composition comprising composition designated NBGM1/HIL A pharmaceutical composition comprising constitutes are useful in the diagnosis, imaging and creatment of neoplastic disease, particularly, melanoma, breast coarcinoma, lung carcinoma, prostatioma, gastric carcinoma, prostate carcinoma, small cell lung carcinoma, neuroblastoma, glioma, soft tissue sarcoma, small cell lung carcinoma, prostatic adenocarcinoma, soft call lymphomas and chronic leukaemias. Hil DNA is also used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                              Human; monoclonal antibody; Mab; H11; single chain variable region; scFv; neoplastic disease; melanoma; immunoglobulin IgM; gene therapy; lymphoma; carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine; neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             soft tissue sarcoma, small cell lu
B and T cell lymphomas and chronic
vaccines and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition comprising antigen binding fragments of recognizes an antigen on neoplastic cells but not or in diagnosis, imaging and treatment of carcinomas.
                                                                                                                                                                                                                                                                                                                                 Human H11-single chain variable region (scFv) complementary
                                                                                                                                                                                                                                                                                                                                                                  04-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD04540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                  C-antigen; chronic
                                    (VIVE-) VIVENTIA BIOTECH INC.
                                                                                                   22-MAY-1997;
                                                                                                                                    27-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCACTAATGGTGATGGTTCAGATCTTCTTCGCTGATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maiti PK,
     Maiti PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 867 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Col 67-70; 56pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence encodes human monoclonal antibody (Mab),
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                    96US-00657449
                                                                                                   97US-00862124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaplan HA
   Kaplan HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33.8; Di
Pred. No. 0.24
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               î.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an antibody that
n normal cells for use
                                                                                                                                                                                                                                                                                                                                    DNA #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0

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RESULT 11
ACA62170/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variable region (SCFV) complementary DNA. The invention relates to human conclonal antibody (Mab) H11, H11-(SCFV) single chain variable (V) immunoglobulin of IgM subclass which is specific to C-antigen found to specifically on neoplastic cells and not on normal cells. H11 antibody is an CC specifically on neoplastic cells and not on normal cells. H11 is an CC year old male with a low grade glioma and fused to a human myeloma cell CC inte to produce a hybridoma designated MBGM/H11. A pharmaceutical CC diagnosis, imaging and treatment of neoplastic disease, particularly, carcinoma, breast carcinoma, lung carcinoma, ovarian carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma, lung carcinoma, lung carcinoma, lymphoma carcinoma, carcinoma, gastric carcinoma, prostate carcinoma, lung carcinoma, small cell lung carcinoma, colon carcinoma, glioma, soft tissue sarcoma, small cell lung carcinoma, colon carcinoma, soft tissue sarcoma, small cell lung carcinoma, carcinoma, small cell selection c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                        22-MAY-1996;
22-MAY-1997;
(DANM/) DAN M
                                                                                                                                                    30-JAN-2003
                                                                                                                                                                                               US2003021779-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glioma; soft tissue sarcoma; small ce
C-antigen specific antibody; alphaC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ds; gene; H11; single chain variable region; gene therapy; scFv; neoplasia; tumour; recurrence risk; C-antigen; melanoma; neuroblastoma; glioma; soft tissue sarcoma; small cell lung carcinoma; brain cancer;
                                                                                                    13-FEB-2001; 2001US-00782397
                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-antigen antibody H11 single chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACA62170 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 867 BP; 189 A; 241 C; 229 G; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition comprising antigen binding fragments of an antibody that recognizes an antigen on neoplastic cells but not on normal cells for use in diagnosis, imaging and treatment of carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-289584/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA is also used in vaccines and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 TTAGTGGTGATGGTGGTGATGGTTCAGGTCTTCTTCGCTGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 TCACTAATGGTGATGGTGATGGTTCAGATCTTCTTCGCTGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Col 71-72; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is human monoclonal antibody (Mab),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                      96US-00657449
97US-00862124
                                                                                                                                                                                                              /*tag= a
/partial
/partial
/product= "H11 single chain variable region fragment
/transl_except= (pos:853. .834,aa:His-Lys)
/note= "No start or stop codon given"
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.3%;
84.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33.8; DB
Pred. No. 0.24;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment #2 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H11-single chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 12
ADO52300
ID ADO52
XX BONA
XX ANTig
KW Neopl
KW Neopl
KW Singl
XX SING
XX Homo

29-JUL-2004 ADO52300; AD052300

(first entry)

standard;

DNA;

867

single

chain

V region

vaccine;

neoplasia; cancer;

Human antibody H11 scFv complementary DNA #2.

Antigen binding fragment, H chain V region, L chain V region, C-antigen,

ccine; gene therapy; human; fragment; scFv; gene; ds.

13-MAY-2004

US2004091484-A1

sapiens

밁 Ş

15 TTAGTGGTGATGGTGATGGTTCAGGTCTTCTTCGCTGATCAG 59

rcáctaardordardordardorreadaretrecitederdaread 817

Matches Query Match Best Local (

38;

Conservative

0

7;

0 Gaps

0

U; 0 Other; Length 867; Indels

Score 33.8; DB Pred. No. 0.24; 0; Mismatches

Similarity

57.3%,

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cc fragment of a monoclonal antibody specific for an antigen binding complastic cells. The antigen binding fragment (ABF) is useful for treating a patient with a neoplasia. The individual has a clinically content of the tumour. The method is useful for palliating the neoplasia. The individual has a clinically content of the antigen binding fragment (ABF) is useful for palliating the neoplasia. The method is useful for palliating the neoplasia. The method is useful for palliating the neoplasia. The content of a clinically detectable tumour. Cc as radioisotopes or immunomodulators. ABF is useful for detecting C-c antigen in a sample. The polypeptide is useful for diagnosing, localising conditions of the sum of the polypeptide is useful for manufacturing novel respents and for treating and imaging composition is useful for eliciting an immune response against neoplasia. Cc rantigen specific antibody, termed Hil or alphaC, as hybridisation of composition is useful for eliciting an immune response against neoplasia. Cc cantigen specific antibody, termed Hil or alphaC, as hybridisation of composition as sample, as primers to effect amplification of desired compositions including vaccines and compositions including vaccines and composition as a polynucleotide is also useful for genetically composition are useful for detecting contering cells in vivo, thus treating various types of cancer. The composition fragment, scFv, #2 DNA continued to the numan C-antigen specific antibody Hil single chain
             Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel antigen binding fragment of monoclonal antibody specific for antigen detected on neoplastic cells, useful for diagnosting or tree cancer, for manufacturing novel reagents and as diagnostic and image
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 7; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dan MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MAIT/)
(KAPL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAITI P K.
KAPLAN H A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU10487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maiti PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaplan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating imaging
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RESULT 13
AD052298/c
ID AD0522
XX AD0522
XX AD0522
XX AD0522
XX Antige
KW Antige
KW neopla
XX Homo s
XX Homo s
XX Homo s
XX ISPH Key
FT CDS
FT CDS
FT CDS
FT Y
XX US2004
PN 13-MAY
XX 29-AUG
PR 22-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a composition comprising an antigen binding fragment of an antibody comprising H Chain V region and L chain V region that specifically recognises C-antigen. The invention is useful for treating a patient with a neoplasia. The antigen binding fragment of the antibody is used as diagnostic and imaging reagents. The invention is useful for genetically altering cells in vivo, to treat various types of cancer. It is also useful in vaccine and gene therapy. The present sequence is human antibody H11 single chain V region fragment (scFV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition useful for treating neoplasia in patient, comprises antigen binding fragment of antibody specifically recognizing C-antigen recognized by antibody comprising H chain V region and L chain V region.
                                                                                                                                                                                                                        Antigen binding fragment; H chain V region; L chain V neoplasia; cancer; vaccine; gene therapy; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 867 BP; 189
                      29-AUG-2003;
                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                     29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complementary DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-399136/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dan MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MAIT/)
(KAPL/)
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22-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-2003;
 22-MAY-1996;
                                               13-MAY-2004.
                                                                                                                                                                                                                                                             Human antibody Hll scFv DNA
                                                                                                                                                                                                                                                                                                                                   ADO52298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2001;
                                                                      US2004091484-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GRAD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DANM/)
                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAN M D.

MAITI P K.

KAPLAN H A

GRAD C.
                                                                                                                                                                                                                chain
                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; SEQ ID NO 18;
                                                                                                                                                                                                                                                                                                                                   standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                         TTAGTGGTGATGGTGGTGATGGTTCAGGTCTTCTTCGCTGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maiti PK,
                                                                                                                                                                                                                                                                                                                                                                                              TCACTAATGGTGATGGTTCAGATCTTCTTCGCTGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-00782397
                      2003US-00651453
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-00657449
97US-00862124
 96US-00657449
                                                                                                                                                                                                             region fragment; scFv;
                                                                                          /product= "Human ;
/transl_except= (|
/partial
/note= "No start ;
                                                                                                                                                               Location/Qualifiers
                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; 241 C;
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                                                                                                                                                                                                                                                                                                                                   867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56pp; English.
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                                                                                                                                                                                                                                                             #2.
                                                                                                                                                                                                                                                                                                                                   ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.24
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33.8;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 G;
                                                                                                                 n antibody |
(pos:853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grad
                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O
                                                                                           stop codon
                                                                                                                                                                                                             gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                             H11 SCFV
                                                                                                                 .864,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                 aa:His-Lys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                     region;
                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  867;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                      C-antigen;
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RESULUT 14
ABK97798/c
ID ABK9777
XX ABK9777
AC ABK977
XX O7-OCT
XX
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; virucide; hepatotropic; antiinflammatory; neuroprotective; immunosuppressive; antiarthritic; cytokine receptor; interferon; IFN; cancer; haematological malignancy; viral infection; hepatitis; human; multiple sclerosis; autoimmune disease; arthritis; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition useful for treating neoplasia in patient, comprises antigen binding fragment of antibody specifically recognizing C-antigen recognized by antibody comprising H chain V region and L chain V region
                                                                            WPI; 2002-547689/58
P-PSDB; ABG68848.
                                                                                                                                                                                                                                                           01-DEC-2000; 2000US-00727388
                                                                                                                                                                                                                                                                                                         30-NOV-2001; 2001WO-CA001701.
                                                                                                                                                                                                                                                                                                                                                              06-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                             WO200244197-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C219scFv DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK97798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK97798 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 7; SEQ ID NO 16; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dan MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DANM/)
(MAIT/)
(KAPL/)
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13-FEB-2001;
                                                                                                                                                                                                         (FISH/)
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MAITI P K.
KAPLAN H A
GRAD C.
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84.4%;
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Pred. No. 0.
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Cytokine receptor binding peptide construct, in particular interferon receptor binding peptide construct for use as an interferon mimetic,

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RESULT 15
AAV10118/c
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Best Local S
Matches 38
   22-MAY-1996;
                                                           22-MAY-1997;
                                                                                                                   27-NOV-1997.
                                                                                                                                                                              WO9744461-A2
                                                                                                                                                                                                                                                                     intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H11; monoclonal antibody; MAb; C-antigen; variable region heavy chain; V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe; primer; vaccine; gene therapy; glioblastoma; neuroblastoma; malignant melanoma; adenocarcinoma; small cell lung carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human H11-scFv construct monomer forming DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 885 BP; 223 A; 227 C; 242 G; 193 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            malignant melanoma; adenocarcinoma; small cell lung carcinoma; single chain variable region; scFv; ss.
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96US-00657449
                                                    97WO-US008962
                                                                                                                                                                                                                                                        /"tag= a /product= "H11-scFv construct" /note= "partial sequence of monomer interrupted by an intron."
                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Pred. No. 0
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(NOVO-) NOVOPHARM BIOTECH INC

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Best Local
                                                                                                                                                                                          This sequence encodes a human H11 monoclonal antibody single chain V region fragment (H11-scFv) construct which is capable of forming monomers. This construct is used to determine the ability of H11-scFv antibody fragments to bind specifically to the C-antigen on cancer cells. Such antigen binding fragments may be used for treating a patient with neoplasia. It is especially useful in the detection of lymphomas and leukaemias where the tumour cells bearing the C antigen are circulating in the patients bloodstream. The polynucleotide sequence may be used as a primer or a probe and the encoded protein may be used in a vaccine or for gene therapy. The human monoclonal antibody (MAD), designated H11, specifically recognises cancerous cells. H11 is specific for glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma and proteirs adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and proteirs adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen binding fragment from monoclonal antibody, H11 - allows tumour specific detection and treatment of neoplasia.
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                                                                                         Similarity
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                               TTAGTGGTGATGGTGATGGTTCAGGTCTTCTTCGCTGATCAG 59
TCACTAATGGTGATGGTTCAGATCTTCTTCGCTGATCAG
                                                                                                                                            918 BP; 213 A; 240 C; 264 G; 201 T; 0 U; 0 Other;
                                                                                                                                                                                 adenocarcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 90-91; 126pp;
                                                                          Conservative
                                                                                       57.3%;
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Search completed: May 19, 2006, 00:53:19 time : 284.094 secs

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59
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1392.544 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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45.4	45.4	45.4	45.4	45.4	45.4	45.4	45.4	45.4	45.4	45.4	45.4	45.8	45.8	45.8	45.8	45.8	45.8	45.8	46.4	46.4	46.4	46.4	46.4	46.4	46.4
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ALIGNMENTS

#### ACCESSION VERSION KEYWORDS SOURCE JOURNAL COMMENT REFERENCE AUTHORS RESULT 1 BI718942/c FEATURES DEFINITION TITLE ORGANISM source DCMB Box 91000 Duke University Durham, NC 27708-1000 Tel: 919 613 8159 Fax: 919 613 8177 BI718942 BI718942.1 GI:15694637 EST. Chlamydomonas reinhardtii Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Chlamydomonadales; Chlamydomonadaceae; Chlamydomonadales. Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in BI718942 687 bp mRNA linear EST 19-SE 1031033C05.yl C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence. Unpublished (2001) Contact: Charles Hauser Vascular Plants. Project: (bases 1 to 687) chauser@duke.edu /note="Vector: pBluescript II SK-; Site\_1: EcoRI; Site\_2: XhoI; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant Phys. 12: 127-135; TAP + H202 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). /strain="CC-1690 wild type mt+ 21gr" /db\_xref="taxon:3055" /clone\_lib="C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II" Location/Qualifiers 1. .687 organism="Chlamydomonas reinhardtii" |mol\_type="mRNA" EST 19-SEP-2001

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JOURNAL
COMMENT
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AUTHORS
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ORGANISM
                                                                                                         Query Match
Best Local (
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Best Local :
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                                 142
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                                                                                          l Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                           FORWARD: TAA TAC GAC TCA CTA TAG GG BACKWARD: CAC TCA TTA GGC ACC CCA Plate: 0002 row: A column: 12 Seq primer: CAC TCA TTA GGC ACC CCA Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza rufipogon
Oryza rufipogon
Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaaee; Oryza.
1 (bases 1 to 319)
Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3', genomic CL793048 CL793048.1 (GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                          PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMAP project
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR_CBa0002A12.r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCTAGGTCGACTCATTAGTGGTGATGGTGGTGGTTCATGGTCTTCTTC 50
                   CTAAACAATAGTGGTGGTGGTGGTGGTTCTGCTGATCATCATCATCA
                                           CGACTCATTAGTGGTGATGGTGGTGATGGTTCAGGTCTTCTTCGCTGATCA 58
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                                                                                       48.5%;
llarity 72.5%;
Conservative
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                                                                                                                                                    /organism="Oryza rufipogon"
/mol type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR CBa0002A12"
/tissue_type="young leaves"
/dev_stage="2 week old seedlings"
/lab_host="0H10B T1 phage resistant"
/clone_lib="OR_CBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XinoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:51015064
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                                                                                  ; Score 28.6; D:
; Pred. No. 64;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
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Pred. No. 45;
0; Mismatches
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                                                                                                             DB 13;
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                                                                                    14;
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ne OR_CBa0002A12
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                                                                                                                                  SOURCE
ORGANISM
                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
                                                                        REFERENCE
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LOCUS
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ORGANISM
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CW656232/c
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VERSION
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JOURNAL
                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                   203
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                                                                                                                                                                GSS
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Query Match
Best Local Similarity
      Oryza rufipogon
Oryza rufipogon
Oryza rufipogon
Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 718)
Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Tartty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
OMAP project
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                OR_CBa0065E21.r OR_CBa Oryza
3', genomic survey sequence.
CL838893
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                                                                                                                                                                                                                                                                                                                                              CL838893
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Oryza glaberrima
Dukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophy
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 406)
Kim,H., Yu,Y., Wissotski,M., Byrne,M., Stum,D., Smart,D., Rao,K
Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3', genomic
CW656232
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OG_BBa0006N20.r OG_BBa Oryza glaberrima genomic clone OG_BBa0006N20
3', genomic survey semmence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="young leaves"
/lab_host="DH10B T1 phage resistant"
/clome lib="OG_BBa"
/note="Vector: pagibac1; Site_1: HindIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza glaberrima"
/mol_type="genomic DNA"
/db_xref="taxon:4538"
/clone="OG_BBa0006N20"
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                                                                                                                                                                                                                                                         GI:51084503
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76.1%;
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Pred. No. 77;
0; Mismatches
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a; Poales; Poaceae; BEP
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P OR_CB#0065E21
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REFERENCE
AUTHORS
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VERSION
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CL796515/c
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                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, A:
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 CAATAGTGGTGGTGGTGGTTCTGCTGTTAGTCCATCATCA 85
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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Forbes Building Room 303, Tucson,
Tel: 520 626 5595
Fax: 520 621 1259
                                                                                                                                                           FORWARD: TAA TAC GAC TCA CTA TAG GG BACKWARD: CAC TCA TTA GGC ACC CCA Plate: 0006 row: K column: 21 Seq primer: CAC TCA TTA GGC ACC CCA Class: BAC ends.
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BACKWARD: CAC TCA TTA GGC ACC CCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arizona Genomics Institute
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                                                                                                                                                                                                                                                                                                                       PCR PRimers
                                                                                                                                                                                                                                                                                                                                          Email: rwing@genome.arizona.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="OR_CBa0065E21"
/tissue_type="young leaves"
/dev_stage="2 week old seedlings"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OR_CBa"
/note="Vector; pAGIBAC1; Site_1: Hind
/note="Vector; pAGIBAC1; Site_1: Hind
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drk treated 36 hrs before harvest"
      /organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
                                                                                                                           Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:4529"
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76.1%;
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Pred. No. 83;
0; Mismatches
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• OR_CBa0006K21
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                                                                                                                                                                                                                 Seq primer: M13 Reverse.
Location/Qualifiers
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Contact: Kerlavage, AR
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1 (bases 1 to 550)
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AA305848
AA305848.1 GI:1958400
                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics
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                                      /db_xref="ATCC (inhost):160223"
/db_xref="taxon:9606"
/cell_type="T-lymphocyte"
/cell_type="T-lymphocyte"
/clone_lib="Jurkat T-cells VI"
                                                                                                                                                           organism="Homo sapiens"
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Pred. No. 8
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/tissue_type="young leaves"
/dev stage="2 week old seedlings"
/lab_nost==DH10B T1 phage resistant"
/clone lib="OR_CBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"
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203 CAATAGTGGTGGTGGTGGTTCTGCTGTTAGTCCATCATCA 158
             13 CATTAGTGGTGATGGTGATGGTTCAGGTCTTCTTCGCTGATCA 58
                                                   Mismatches
                                                                                DB 13;
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                                                                                Length 746;
                                                    Indels
                                                    <u>,</u>
                                                    Gaps
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RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Balt, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Barle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Pields, C., Fraser, C.M. and Venter, J.C.
Email: arkerlav@tigr.org
For clone availability, additional sequence and exinformation related to this EST, please check the Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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EST177056 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA
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he TIGR Human Gene
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CF131918
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                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               http://genome.uiowa.edu/distribution/humanfl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Mary Hendrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Iowa 375 Newton Road , 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coordinated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Normalization and subtraction: two approaches to discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF131918 689 bp mRNA linear UI-HF-FQO-aws-i-23-0-UI.rl NIH_MGC_215 Homo sapiens IMAGE:30553846 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library preparation: Dr. M. Bento Soares, University of CDNA Library Arrayed by: Dr. M. Bento Soares, University of I DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.
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      TGGTGATGGTGATGGTTCAGGTCTTCTTCGCTGATCAG 59
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319 335 9565
1. hore-
                                                                                                      /clone="MAMGE:3053846"
/clone="MAMGE:3053846"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_hoSt="DH10B (T1 phage resistant)"
/clone_lib="NTH MGC 215"
/clone_lib="NTH MGC 215"
/note="Organ: Lung, Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
BonaIdo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATMAAGGCCA. Tissue was provided by Mary Hendrix."
                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:9606"
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XhoI"
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                                                         47.8%;
80.5%;
                                                                                                                                                                                                                                                                                                                                                                        type="mRNA"
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80.5%;
                                        Score 28.2; D
Pred. No. 97;
0; Mismatches
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Pred. No. 94;
0; Mismatches
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                                                                    DB 5;
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80.5%;
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BH742923 585
gz67d03.gl BoBuds01 Brassica
genomic survey sequence.
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-APR-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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/note="Genoscope sequence
end : PUC-Ori"
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"mol type="genomic DNA"

/db xref="taxon:99883"

/clone="103C12"
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nigroviridis genome survey sequence PUC-Ori end
library G from Tetraodon nigroviridis, genomic
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Pred. No. le+02;
0; Mismatches
                     bp DNA linear GSS 25-FEB-2002
oleracea genomic clone gz67d03 5',
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Other_GS
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Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 794)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mccombie@cshl.org
Plate: gz67 row: d column:
Seq primer: -21UnivRev
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1 (bases 1 to 585)

Katari,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J., Bahija,V., Cunnius,D.M., Katzenberger,F., King,L., Kirchoff,K., Kuit,K., Miller,B., Muller,S., Nascimento,L., Preston,R., Santos,L., Shah,R., Zutavern,T., Dedhia,N., Rabinowicz,P.D. and McCombie,W.R.
                                                                                                      Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D. Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
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Location/Qualifiers
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Fax: 516 367 8874
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                                            Contact: Chris Town
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Medical Center Drive, Rockville,
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                                                                 GSSs: BOGSI92TF
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone="9267d03"
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Pred. No. 1.1e+02;
0; Mismatches 10
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32; Conserv
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Unpublished (2002)
Contact: BHALERAO RUPALI R.
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus. 1 (bases 1 to 722)
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Populus tremula
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Class: sheared ends
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DNA is from a doubled haploid provided by Tom Osborn.
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                       Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea,
                                                                                                                                                                                                                                                                                                                                                                                  Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
The poplar tree transcriptome: Analysis of expressed sequence tags
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CATAAGTGGTGGTGGTGGTTGAAGTCTCCTTAG 349
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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/db_xref="taxon:113636"
/tissue_type="petioles"
/clone_lib="Populus petioles
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/clone="BOGSI92"
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library Populus tremula
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1.3e+02;
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RESULT 12 DN496361/c LOCUS

DN496361

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                                        Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seedun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
                                                                                                                                                                Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Cpark,J.Y., Lim,M.H., Kim,H.I., Lim,Y.P. and Park,B.S. End sequence of Brassica rapa HindIII BAC library (KE Unpublished (2004)
                                                                                                                                                                                                                                                     Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                 Contact: Beom-Seok Park
                                                                                                                                                                                                                                                                                                                                                                        CW980355.1 GI:56811642 GSS.
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32; Conserv
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Sterky, F., Bhalerao, R.R., Unneberg, P., Segerman, B., Nilsson, P., Brunner, A.M., Charbonnel-Campaa, L., Lindvall, J.J., Tandre, K., Strauss, S.H., Sundberg, B., Gustafsson, P., Uhlen, M., Bhalerao, R.P., Nilsson, O., Sandberg, G., Karlsson, J., Lundeberg, and Jansson, S. A. Populus EST resource for plant functional genomics proc. Matl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: bo.segerman@plantphys.umu.se.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_ESTs: P061G11, P061G11.3pR
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pbeom@rda.go.kr
i sequence of Brassica rapa ssp.
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/mol_type="mRNA"
/db_xref="taxon:113636"
/clone="P061G11"
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/clone_lib="Populus pet
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HindIII BAC library Brassica rapa
KBrH004J05, genomic survey
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CX110631 271 bp mRNA linear BI050P21 A normalized whole-life-cycle cDNA library sativa (indica cultivar-group) cDNA clone BI050P21 :
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Sus scrofa
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Submitted (01-NOV-2005) The Sanger Institute, w
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                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was generated from the T7 end of BAC 19E6. 19E6 is part of the CHORI-242 BAC Library created by P. de Jong. Further details: http://www.sanger.ac.uk/Projects/S_scrofa/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campus, Hinxton, Cambridgeshire, (humquery@sanger.ac.uk Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CTAGGTCGACTCATTAGTGGTGATGGTGGTGATGGTTCAGGTCTTCTTCGCTGATCAG 59
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                                                                                                                                                                                                                                                              /mol_type="genomic_DNA"
/db_xref="taxon:9823"
/clome="CH242-1986"
/tissue_type="White_blood_cells"
/note="Vector_pTARBAC1.3_BamHI
sex_female"
                                                                                                                                                                                                                                                                                                                                                          organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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/lab host="E.coli DH10B"
/clone_lib="KBrH, Brassica rapa HindIII BAC library"
/note="Vector: pCUGIBac1; Site_1: HindIII; Brassica rapa
spp. pekinensis inbred line Chlifu BAC library (KBrH BAC)
is provided by Yong-Pyo Lim."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrH004J05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic
/cultivar="Chiifu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laurasiatheria; Cetartiodactyla;
                                                                                                                                                                             Score 27.6; DB 14;
Pred. No. 1.6e+02;
0; Mismatches 9;
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Pred. No. 1.5e+02;
0; Mismatches 19;
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. E-mail enquiries:
                                                                                                                                                                                                             923;
EST 03-JUN-2005
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Search completed: May 19, 2006, 02:31:57 Job time : 2372.22 secs
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Zhang, J., Feng, Q., Jin, C., Qiu, D., Zhang, L., Xie, K., Yuan, D.,

Han, B., Zhang, Q. and Wang, S.

Features of the expressed sequences revealed by a large-scale analysis of ESTs from a normalized cDNA library of the elite indica rice cultivar Minghii 63

Plant J. 42 (5), 772-780 (2005)
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CX110631
CX110631.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wang S
National Key Laboratory of Crop Genetic Improvement
Hauzhong Agricultural University
Wuhan 430070, China
Tel: 86-27-87282044
Fax: 86-27-87287092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Foales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: shipingwang@hotmail.com
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                            /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; The library is constructed based on the strategy of satuation hybridization with genomic DNA using rice cultivar Minghui 63. This library consists of cDNA from 15 directionally cloned cDNA libraries constructed with different tissues from 9 developmental stages."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
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/dev_stage="whole-life-cycle"
/dev_stage="whole-life-cycle"
/lab_host="E. coli DH10B"
/clone_lib="A normalized whole-life-cycle cDNA library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Listing first 45 summaries
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/EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

/EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

/EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

/EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

/EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

/EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

/EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

/EMC_Celerra_SIDS3/ptodata/2/ina/PD_COMB.seq:*

/EMC_Celerra_SIDS3/ptodata/2/ina/BD_COMB.seq:*

/EMC_Celerra_SIDS3/ptodata/2/ina/BD_COMB.seq:*

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-92-037-5
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Sequence Sequence Sequence	Sequence Sequence Sequence			Sequence Sequence Sequence	Sequence Sequence	Sequence Sequence	Sequence Sequence	Sequence Sequence
13, Appl 13088, A 11796, A	5216, Ap 13254, A 12705, A	48, Appl 5247, Ap	1, Appli 1302, Ap 47, Appl	568, App 13, Appl 1, Appli	43, Appl 47, Appl	5,5	4, Appli 9516, Ap	38, Appl 4, Appli

## ALIGNMENTS

US-08-872-485-8 GENERAL INFORMATION:
APPLICANT: Gilbert
APPLICANT: Wakarch
APPLICANT: Young, I
APPLICANT: Jenning Sequence 8, Patent No. APPLICATION NUMBER: US/08/872,485
FILING DATE: 07-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,520
FILING DATE: 10-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REGISTRATION NUMBER: 35,367 REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8: ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: SEQUENCE CHARACTERISTICS: LENGTH: 63 base pairs CORRESPONDENCE ADDRESS: TITLE OF INVENTION: Recombinant alpha-2,3-Sialyltransferases TITLE OF INVENTION: and Their Uses NUMBER OF SEQUENCES: MOLECULE TYPE: TOPOLOGY: STRANDEDNESS: ADDRESSEE: , Application 6096529 San Francisco nucleic acid EDNESS: single California E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor Jennings, Micheal P. Wakarchuk, Warren W. Young, N. Martin Gilbert, Michel USA US/08872485 œ 014137-012000US

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US-09-387-942-8
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US-09-387-942-8
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; OTHER INFORMATION:
US-08-872-485-8
                                                                      Matches
                                                                                                                                                                                                                                                                             NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 0141
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                  MOLECULE TYPE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jennings, Micheal P.
TITLE OF INVENTION: Recombinant alpha-2,3-Sialyltransferases
TITLE OF INVENTION: and Their Uses
                                                                                                                                     NAME/KEY:
LOCATION: 1..63
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Californ:
                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                        LENGTH:
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: nucleic acid
NDEDNESS: single
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5. 6210933
                                                                                 Similarity
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                     CCTAGGTCGACTCATTAGTGGTGATGGTGATGGTTCAGGTCTTC 47
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                                                                Conservative
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Young, N. Martin
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                                                             Score 37.4; DB 3;
Pred. No. 0.00082;
0; Mismatches 6;
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Pred. No. 0.00082;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/058,636
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US/09/272,960
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 60/078,891
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 7
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APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wational Research Council of Canada
TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase
TITLE OF INVENTION: Campylobacter jejuni and Its Uses
FILE REFERENCE: 014137-013210US
                                                                                           Matches
                                                                                                         Query Match
Best Local
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Best Local Similarity
Matches 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                        LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase
TITLE OF INVENTION: Campylobacter jejuni and Its Uses
FILE REFERNCE: 014137-0112210US
FILE REFERNCE: 014137-012210US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Artificial Sequence
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ilarity 85.1%;
Conservative
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85.1%;
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Pred. No. 0
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Pred. No. 0.0029;
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APPLICANT: Wood, Kenneth
APPLICANT: Piner, Jeffrey
APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Mak, John
APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: Methods of screening for modulators of
TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
TITLE OF INVENTION: proliferation states
TITLE OF INVENTION: proliferation states
FILE REFERENCE: 1014A
CCURRENT APPLICATION NUMBER: US/09/724,519
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/52,037
PRIOR APPLICATION NUMBER: 09/428,156
PRIOR APPLICATION NUMBER: 09/428,156
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
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                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-09-592-037-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wood, Kenneth
APPLICANT: Finer, Jeffrey
APPLICANT: Beraud, Christ
APPLICANT: Mak, John
APPLICANT: Sakowicz, Roma
APPLICANT: Sakowicz, Roma
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Patent No. 6414121
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                                                                              Matches
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                                                                                                                      Query Match
                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/592,037
CURRENT FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: 09/428,156
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Methods of screening for modulators of TITLE OF INVENTION: cell proliferation and methods of diagnosing cell TITLE OF INVENTION: proliferation states
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SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Human
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                                12 TCATTAGTGGTGATGGTGATGGTTCAGGTCTTCTTCGCTGATCAG 59
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Sakowicz, Roman
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Beraud, Christo
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83.3%;
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                                                                            Score 35.2; DB 3;
Pred. No. 0.0094;
0; Mismatches 8;
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Sequence 3, Application US/09428156B;
Patent No. 6617115;
GENERAL INFORMATION:
APPLICANT: Wood, Kenneth
APPLICANT: Finer, Jeffrey
APPLICANT: Beraud, Christophe
APPLICANT: Mak, John
APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: Methods of screening for modulators of
TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
TITLE OF INVENTION: proliferation states
FILE REFERENCE: CYTOP033;
CURRENT APPLICATION NUMBER: US/09/428,156B;
CURRENT APPLICATION NUMBER: 1999-10-27;
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
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; ORGANISM: Human
US-09-428-156B-3
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                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 5
LENGTH: 1542
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Patent No. 6414121
                                                                           Matches
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Best Local Similarity
                                                                                                             Query Match
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APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: Methods of screening for modulators of
TITLE OF INVENTION: cell proliferation and methods of diag
TITLE OF INVENTION: proliferation states
FILE REFERENCE: 1014A
CURRENT APPLICATION NUMBER: US/09/724,519
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/592,037
PRIOR APPLICATION NUMBER: 09/428,156
PRIOR APPLICATION NUMBER: 09/428,156
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APPLICANT: Finer, Jeffrey
APPLICANT: Beraud, Christophe
                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-10-27
                                                                                                                                                                    TYPE: DNA ORGANISM: Human
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1149 TCAGTGGTGGTGGTGGTGCTCGATCAGGTCCTCCTCGCTGATCAG 1102
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83.3%;
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                                                                                       Score 35.2; DB Pred. No. 0.01;
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Pred. No. 0.0094;
0; Mismatches
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RESULT 9 US-09-592-037-5/c

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CURRENT APPLICATION NUMBER: US/09/428,156B
CURRENT FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 5
LENGTH: 1542
TYPE: DNA
ORGANISM: Human
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APPLICANT: Wood, Kenneth
APPLICANT: Finer, Jeffrey
APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Mak, John
APPLICANT: Sakowicz, Roman
ITILE OF INVENTION: Methods of screening for modulators of
ITILE OF INVENTION: proliferation and methods of diagnosing cell
ITILE OF INVENTION: proliferation and methods of diagnosing cell
ITILE REPERENCE: 10144
FILE REPERENCE: 10149
FILE REPERENCE: 1
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                            GENERAL INFORMATION: APPLICANT: Beraud,
                                                                                            Sequence 3, Application US/09592054 Patent No. 6440684
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      APPLICANT:
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GENERAL INFORMATION:
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Best Local :
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LENGTH: 1542
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APPLICANT: Finer, Jeffrey
APPLICANT: Beraud, Christophe
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40; Conserv
Beraud, Christophe Finer, Jeffrey
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Sakowicz, Roman
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Pred. No. 0.01;
0; Mismatches 8;
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GENERAL INFORMATION:
APPLICANT: Wood, Kenneth
APPLICANT: Finer, Jeffrey
APPLICANT: Beraud, Christ
APPLICANT: Mak, John
APPLICANT: Sakowicz, Roma
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US-09-592-037-7/c
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US-09-724-519-7/c
; Sequence 7, Applica
; Patent No. 6414121
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US-09-724-519-7
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                                                                                                                                                            Sequence 7, Application US/09592037 Patent No. 6437115
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Best Local Similarity
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SEQ ID NO 7
ELENGTH: 1728
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APPLICANT: Finer
APPLICANT: Berau
APPLICANT: Mak,
APPLICANT: Sakov
APPLICANT: Beraud, Christophe
APPLICANT: Mak, John
APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: Methods of screening for modulators of
TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
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APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6440684el motor proteins and methods
TITLE OF INVENTION: their use
FILE REPERENCE: 1016
CURRENT APPLICATION NUMBER: US/09/592,054
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Methods of screening for modulators of
TITLE OF INVENTION: cell proliferation and methods of diagnosing
TITLE OF INVENTION: proliferation states
FILE REFERENCE: 1014A
CURRENT FAPPLICATION NUMBER: US/09/724,519
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/592,037
PRIOR APPLICATION NUMBER: 09/592,037
PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: 09/428,156
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 10
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TYPE: DNA
ORGANISM: Human
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Beraud, Christophe
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Beraud, Christophe
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TITLE OF INVENTION:

proliferation states

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US-08-862-124-16/c
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; ORGANISM: Human
US-09-428-156B-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09428156B Patent No. 6617115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 59.7%;
Best Local Similarity 83.3%;
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SEQ ID NO 7
LENGTH: 1728
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Best Local Similarity
Matches 40; Conserv
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APPLICANT:
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ORGANISM: Human
-09-592-037-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/428,156
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Methods of screening for modulators of TITLE OF INVENTION: cell proliferation and methods of diagnosing TITLE OF INVENTION: proliferation states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 1014A
CURRENT APPLICATION NUMBER: US/09/592,037
CURRENT FILING DATE: 2000-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/428,156B
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                                                                                                                                                                            APPLICANT: Dan, Michael D.
APPLICANT: MaitL Pradip K.
APPLICANT: MaitL Pradip K.
APPLICANT: MaitL Pradig K.
APPLICANT: Michael D.
APPLICANT: MaitL Pradig K.
APPLICANT: M
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                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP STREET: 755 Page Mill Road CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1728
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Sakowicz, Roman
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                                                                                                                                                                            ANTIGEN BINDING FRAGMENTS H11, THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
DETECTION OF CANCERS
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83.3%;
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US-08-862-124-16
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                       LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (650, C. TELEPHONE: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/01
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                       TOPOLOGY:
                                                   861 TCACTAATGGTGATGGTGATGGTTCAGATCTTCTTCGCTGATCAG 817
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                                                                                    TTAGTGGTGATGGTGATGGTTCAGGTCTTCTTCGCTGATCAG 59
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Search completed: May 19, Job time : 94.6458 secs

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Minimum
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Perfect score:
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| EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11E_PUBCOMB.seq:*
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          US-09-211-691-6
US-10-317-773-6
US-10-317-428-6
US-10-058-636-4
US-10-09-016-4
US-10-601-036-5
US-10-601-036-7
US-09-782-397-18
US-09-782-397-15
US-10-651-453-15
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713.619 Million cell updates/sec
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Biocceleration Ltd.
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107613	38646	4068	393	1782	1659	1634	1634	1176	1176	1176	600	600	23407	975	669	1079	1113	1086	1080	72	72	1817	1817	1977	1906	1806	705
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US-10-333-069-1	US-10-085-117-193	5-115-	US-10-425-115-115233	US-10-739-930-4399	US-10-282-122A-13971	US-10-305-720-1302	US-10-352-684A-19	US-10-925-095-568	US-10-225-567A-311	US-09-826-509-568	US-11-060-756-6389	US-11-060-756-2117	US-11-097-143-7663	US-10-437-963-93368	US-10-739-930-1508	US-10-352-839-4	US-10-335-394-38	US-10-335-394-36	US-10-335-394-39	US-10-380-926-13	US-10-335-394-25	US-10-489-626-6	US-10-489-626-4	US-10-380-438-2	US-10-491-653-25	US-10-380-438-4	US-10-488-374-3
Sequence 1, Appli	Sequence 193, App		e 115233		e 13971,	1302	19,	Sequence 568, App	311,	Sequence 568, App	6389,	2117,		93368,	Sequence 1508, Ap	Sequence 4, Appli	Sequence 38, Appl	Sequence 36, Appl		Sequence 13, Appl	25,	•	Sequence 4, Appli	Seguence 2, Appli	Sequence 25, Appl	Sequence 4, Appli	Sequence 3, Appli

## ALIGNMENTS

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RESULT 2
US-10-317-773-6
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US-09-211-691-6
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Best Local S
Matches 59
Sequence 6, Application US/10317773 Publication No. US20030180928A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09211691 Patent No. US20020034805A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/211,691
CURRENT FILLING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: US 60/069,443
PRIOR FILING DATE: 1997-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gilbert, Michel
APPLICANT: Young, N. Martin
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Pusion. Proteins for Use in
TITLE OF INVENTION: Oligosaccharides
FILE REFERENCE: 019957-012910US
                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:SIALM-23R 3'OTHER INFORMATION: primer
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 59
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                  CCTAGGTCGACTCATTAGTGGTGATGGTGGTGATGGTTCAGGTCTTCTTCGCTGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Ver. 2.1
                                                                                                                                          CCTAGGTCGACTCATTAGTGGTGATGGTGATGGTTCAGGTCTTCTTCGCTGATCAG 59
                                                                                                                                                                                                                               100.0%; Score 59; DB 3; ilarity 100.0%; Pred. No. 2.7e-10; Conservative 0; Mismatches 0;
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Sequence 6, Application US/10317428
Publication No. US20030186414A1
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Young, N. Martin
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Mational Research Council of Canada
TITLE OF INVENTION: Nucleic Acid That Encodes a Fusion Protein
FILE REFERENCE: 019633-000811US
CURRENT APPLICATION NUMBER: US/10/317,428
CURRENT FILING DATE: 2002-12-11
PRIOR APPLICATION NUMBER: US 60/069,443
PRIOR FILING DATE: 1997-12-15
US-10-058-636-4
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                      RESULT 4
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US-10-317-428-6
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                                                                                                                                                           Matches
                                                                                                                                                                        Query Match
Best Local &
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SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/211,691
PRIOR FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                FEATURE: TOPORMATION: Description of Artificial Sequence:SIALM-23R OTHER INFORMATION: primer
                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                        Similarity
                                                                                     CCTAGGTCGACTCATTAGTGGTGATGGTGATGGTTCAGGTCTTCTTCGCTGATCAG 59
                                                            CCTAGGTCGACTCATTAGTGGTGATGGTGGTGATGGTTCAGGTCTTCTTCGCTGATCAG
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Pred. No. 2.7e-10;
**icmatches 0;
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                                                                                                                                                                                Length 59
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Sequence 4, Application US/10058636
Publication No. US20030049270A1
GENERAL INFORMATION:
APPLICANT: Glibert, Michel
APPLICANT: Makarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
ITILE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
FILE REFERENCE: 014137-013210US
CURRENT APPLICATION NUMBER: US/10/058,636
CURRENT APPLICATION NUMBER: US/9/272,960
PRIOR APPLICATION NUMBER: US/9/272,960
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: US 60/078,891
PRIOR APPLICATION NUMBER: US 60/078,891
PRIOR APPLICATION NUMBER: US 99/272,960
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: US 99/272,960
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: US 99/272,960
PRIOR FILING DATE: 1999-03-18
SOFTMARDE: DATE: 1999-03-18
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; OTHER INFORMATION: Description of Artificial Sequence:CJ40R 3'
US-10-799-016-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/799,016
CURRENT FILING DATE: 2004-03-11
PRIOR APPLICATION NUMBER: US/10/58,636
PRIOR FILING DATE: 2002-01-29
PRIOR PRIOR DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US/09/272,960
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR PRIOR APPLICATION NUMBER: US 09/272,960
PRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1997-03-18
PRIOR 
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Best Local S
Matches 40
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Publication No. US20040152165A1
GENERRAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
TITLE OF INVENTION: Campylobacter jejuni and Its Uses
FILE REFERENCE: 014137-013210US
CIRPRINT ADDITICATION WINDERS. 114147700 000
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                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 60
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ORGANISM: Artificial Sequence
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nes 40; Conserv
1 CCTAGGTCGACTCATTAGTGGTGATGGTGGTGATGGTTCAGGTCTTC 47
                                                                                                                                             40;
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                                                                                                                                                                                 Similarity
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85.1%;
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                                                                                                                             Score 35.8; DB Pred. No. 0.023; 0; Mismatches
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Pred. No. 0.023; 0; Mismatches
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CCTAGGTCGACTCATTAGTGGTGATGGTGGTGATGTTCCCCCTTTCTC 47

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; TYPE: DNA
; ORGANISM: Human
US-10-601-036-3
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; ORGANISM: Human
US-10-601-036-5
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Best Local Similarity 83.3
                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1542
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APPLICANT: Wood, Kenneth
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                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10601036 Publication No. US20040214249A1
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wood, Kenneth
APPLICANT: Finer, Jeffrey
APPLICANT: Beraud, Christophe
APPLICANT: Mak, John
APPLICANT: Mak, John
APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: Methods of screening for modulators of
TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
TITLE OF INVENTION: proliferation states
FILE REFERENCE: CYTOP033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/601,036

CURRENT FILING DATE: 2003-06-19

PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/428,156B
PRIOR FILING DATE: 1999-10-27
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/601,036
CURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: BRIOR APPLICATION NUMBER: US/09/428,156B
PRIOR FILING DATE: 1999-10-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITILE OF INVENTION: Methods of screening for modulators of TITILE OF INVENTION: cell proliferation and methods of diagnosing cell TITLE OF INVENTION: proliferation states
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1542 TCAGTGGTGGTGGTGGTGCTCGATCAGGTCCTCGCTGATCAG 1495
                                       12
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                                                                                40;
                            TCATTAGTGGTGATGGTGGTGATCAGGTCTTCTTCGCTGATCAG 59
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Beraud, Christophe
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                                                                                Conservative
                                                                                               59.7%;
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                                                                                          Score 35.2; DB 9 Pred. No. 0.064;
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                                                                            Mismatches
                                                                                                                 DB 9;
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                                                                            8; Indels
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                                                                                                                 Length 1542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-601-036-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/10601036 Publication No. US20040214249A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Ap
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/601,036
CURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/428,156B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wood, Kenneth
APPLICANT: Finer, Jeffrey
APPLICANT: Beraud, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Methods of screening for modulators TITLE OF INVENTION: cell proliferation and methods of dTITLE OF INVENTION: proliferation states FILE REFERENCE: CYTOP033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1728
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY/AGENT INFORMATION:
NAME: Lebnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                     ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PStentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT

SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dan, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1728 TCAGTGGTGGTGGTGGTGCTCGATCAGGTCCTCCTCGCTGATCAG 1681
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                                                                                                                                                                       APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09782397
No. US20030021779A1
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Kaplan, Howard A.
                                                                                                                                                                                                                                                                                                                                                                                           USA
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DETECTION OF CANCERS
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TELEX:

TELEFAX: (650) 494-0792

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US-09-782-397-18
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US-09-782-397-18
Sequence 18, Application US/09782397
Publication No. US20030021779A1
GENERAL INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-782-397-16
          Query Match
                                                                             INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENCTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                               APPLICATION NUMBER: 08/862,124
PILING DATE: 1997-05-22
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELEPHONE: (650) 813-5600
TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                   SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS;
ADDRESSE: MORRISON & FOERSTET LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           861 TCACTAATGGTGATGGTGATGGTTCAGATCTTCTTCGCTGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 TTAGTGGTGATGGTGATGGTTCAGGTCTTCCTTCGCTGATCAG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                 TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
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     57.3%;
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   Score 33.8;
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 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.30
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Length 867;
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LS, NUCLEOTIDES ENCODING THE
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GENERAL INFORMATION:

APPLICANT: Maiti, Fradip K.

APPLICANT: Maiti, Fradip K.

APPLICANT: Maiti, Fradip K.

APPLICANT: Maiti, Fradip K.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THATITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRATITLE OF INVENTION: DETECTION OF CANCERS

FILE REFERENCE: 31608200103

CURRENT FILING DATE: 2003-08-29

PRIOR APPLICATION NUMBER: US 09/782,397

PRIOR FILING DATE: 2001-02-13

PRIOR APPLICATION NUMBER: US 08/662,124

PRIOR FILING DATE: 1997-05-22

PRIOR APPLICATION NUMBER: US 08/667,449

PRIOR FILING DATE: 1996-05-22

PRIOR APPLICATION NUMBER: US 08/657,449

PRIOR FILING DATE: 1996-05-22

PRIOR FILING DATE: 1997-05-22

NUMBER OF SEQ ID NOS: 29
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GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
APPLICANT: Maiti, Pradip K.
APPLICANT: Maiti, Pradip K.
APPLICANT: Kaplan, Howard A.
APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: AUTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,
TITLE OF INVENTION: AUTIGEN BINDING THE FRAGMENTS, AND USE THEREOF FOR THE PROPI
TITLE OF INVENTION: DETECTION OF CANCERS
FILE REFERENCE: 316082000103
CURRENT APPLICATION NUMBER: US/10/651,453
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 08/862,124
PRIOR APPLICATION NUMBER: US 08/862,124
PRIOR APPLICATION NUMBER: US 08/657,449
PRIOR FILING DATE: 1997-05-22
PRIOR FILING DATE: 1996-05-22
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; Sequence 16, Application US/10651453
; Publication No. US20040091484A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     문
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Matches
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SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
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OTHER INFORMATION:
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No. US20040091484A1
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Conservative
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84.4%;
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Pred. No. 0.18;
0; Mismatches 7;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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RESULT 13
US-09-782-397-13/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09782397
Publication No. US20030021779A1
GENERAL INFORMATION:
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Best Local 9
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                                       Query Match
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                     TELEX: 706141
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/782,397

FILING DATE: 13-Feb-2001

CLASSIFICATION: CUNKnown>
                  Local Similarity 84.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dan, Michael D.
Maiti, Pradip K.
Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11,
SPECIFICALLY DETECT CANCER CELL
FRAGMENTS, AND USE THEREOF FOR
                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                          LOCATION: join(1..906, 913..918)
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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   38;
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                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                              LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/862,124 FILING DATE: 1997-05-22
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CITY: Palo Alto
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                                                                                                                                                                 TOPOLOGY:
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 Score 33.8; DB 3; Length 918; Pred. No. 0.18; 0; Mismatches 7; Indels
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RESULT 15
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Publication No. US20030021779A1
GENERAL INFORMATION:
                                                                                                                  GENERAL INFORMATION:
                                                                                                                                       Sequence 13, Application US/10651453 Publication No. US20040091484A1
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 38; Conserv
APPLICANT: Dan, Michael D.
APPLICANT: Maiti, Pradip K.
APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,
TITLE OF INVENTION: NUCLECTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Maiti, Pradip K.
Maiti, Pradip K.
Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES EN
SPECIFICALLY DETECT CANCERS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FILE REFERENCE: 316082000103
CURRENT APPLICATION NUMBER: US/10/651,453
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 09/782,397
PRIOR APPLICATION NUMBER: US 09/782,397
PRIOR APPLICATION NUMBER: US 08/862,124
PRIOR FILING DATE: 1997-05-22
PRIOR FILING DATE: 1997-05-22
PRIOR FILING DATE: 1996-05-22
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VERSION 3.1
LENGTH: 918
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1).(906)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (913)..(918)
OTHER TOPORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (913)..(918)
OTHER TAPORMATION:
Search completed: May 19, 2006, 05:02:08 Job time: 1016.91 secs
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                                                                                                                                                    Query Match 57.3%; Score 33.8; DB 8; Length 918; Best Local Similarity 84.4%; Pred. No. 0.18; Matches 38; Conservative 0; Mismatches 7; Indels C
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Minimum
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 length: 0
length: 2000000000
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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 GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd
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                              US-11-217-529-173940
US-11-0488-619-2934
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US-11-075-891-11
US-11-075-891-13
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79752, A
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US-11-217 US-10-511 US-10-511 US-10-861 US-11-301 US-11-301 US-11-217 US-10-861 US-10-861 US-10-861 US-10-861 US-10-861 US-10-861 US-10-861 US-11-217 US-11-217 US-11-217 US-11-217 US-11-217 US-11-217 US-11-217 US-11-217 US-11-217	US-10-10-1861-934-93 US-11-217-529-191160 US-10-511-937-409 US-10-661-934-29 US-11-301-554-785 US-11-301-554-785 US-11-301-554-785 US-11-217-529-2359 US-11-217-529-2359 US-10-514-738-32 US-10-614-738-32 US-10-614-738-32 US-10-61-934-15 US-10-61-934-15 US-10-861-934-25 US-11-217-529-331 US-11-217-529-331 US-11-217-529-331 US-11-217-529-331	1125	1941	1560	1452	1035	969	1677	1623	925	834	8448	3410	2653	1713	6353	5502	2432	1909	1875	476
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Title:

Run on:

## ALIGNMENTS

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APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHHHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Saccharomyces pastorianus US-11-217-529-173940
                                                                                                                                                                                                                                                                                                                                      US-10-488-619-2934/c
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Sequence 2934, Application US/10488619

Publication No. US20060099578A1

GENERAL INFORMATION:

APPLICANT: Greenlee, Winner and Sullivan, P.C.

APPLICANT: Greenlee, Winner and Sullivan, Polymorphisms, Haplogroups, Associations TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations FILE REFERENCE: 98-01 WO FILE REFERENCE: 98-01 WO CURRENT APPLICATION NUMBER: US/10/488,619

CURRENT FILING DATE: 2004-03-01

NUMBER OF SEQ ID NOS: 3040-03.1

SOFTWARE: Patentin version 3.1

SEQ ID NO 2934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 39.0%;
Best Local Similarity 68.1%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.3 SEQ ID NO 173940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 173940, Application US/11217529 Publication No. US20060099612A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 10/932,182 PRIOR FILING DATE: 2004-09-02
                                                                                                                                                                                                                                                                                                                                                                                                                                              554 TAGGTCAATTGGCTATTGGTGTTGGTGCTGATGCCGTTGATGTT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB 7; Pred. No. 5.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
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; TYPE: DNA ; ORGANISM: Mus musculus US-10-488-619-2934

LENGTH:

599

Query Match

Local

Similarity

38.6%;

DB

6

Length

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; ORGANISM: Homo sapiens US-11-301-554-1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/11/301,554
CURRENT FILING DATE: 2005-12-13
PRIOR APPLICATION NUMBER: US 10/283,017
PRIOR FILING DATE: 2002-10-28
PRIOR PILING DATE: 2002-03-29
PRIOR FILING DATE: 2002-03-29
PRIOR PILICATION NUMBER: US 10/017,754
PRIOR PILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 09/902,941
PRIOR APPLICATION NUMBER: US 09/902,941
PRIOR APPLICATION NUMBER: US 09/849,626
PRIOR PILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-07
PRIOR PILING DATE: 2001-05-03
PRIOR PILING DATE: 2001-05-03
PRIOR PILING DATE: 2001-05-03
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Best Local S
Matches 29
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; Sequence 1922, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 2157
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1922
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/671,325
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/658,824
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/736,457
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 09/702,705
PRIOR FILING DATE: 2000-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/677,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: MCNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                  ENGTH: 507
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                                                                                       Local Similarity
les 29; Conserva
                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 TGGCCTCTTCGGTGGTGGTTGTGGTTATGGTTGTTGTTGTTGTTGTT 280
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CCATGGGCGTGGCACCGGTGGTGGTGGTGGTGATGCTGCA 2
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                             CCTAGGTCGACTCATTAGTGGTGATGGTGGTGATGGTTCA 40
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Carter, Darrick
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                                                                                     Conservative
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                                                                                                    38.0%;
72.5%;
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                                                                          Score 22.4; DB 7;
Pred. No. 7.7;
0; Mismatches 11;
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                                                                          11;
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                                                                                                                 Length 507;
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Sequence 7, Application US/11075891
Publication No. US20060088521A1
GENERAL INFORMATION:
APPLICANT: MAHADEVAN, DARUKA
TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
FILE REFERENCE: 263922US96
                                                                                                                         RESULT 6
US-11-075-891-7/c
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Best Local S
Matches 30
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US-11-075-891-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/557,258
PRIOR FILING DATE: 2004-03-27
NUMBER OF SEQ ID NOS: 36
SOPTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/11075891
Publication No. US20060088521A1
GENERAL INFORMATION:
APPLICANT: MAHADEVAN, DARUKA
TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
FILE REFERENCE: 263922US96
CURRENT APPLICATION NUMBER: US/11/075,891
CURRENT FILING DATE: 2005-03-10
CURRENT FILING DATE: 2005-03-10
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CURRENT APPLICATION NUMBER: US/11/075,891
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Publication No. US20060099578A1
GENERAL INFORMATION:
APPLICANT: Greenlee, Winner and Sullivan, P.C.
TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations of TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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SEQ ID NO 1997
LENGTH: 569
                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Synthetic Peptide
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(767)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 98.01 WO CURRENT APPLICATION NUMBER: US/10/488,619 CURRENT FILING DATE: 2004-03-01 NUMBER OF SEQ ID NOS: 3040
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                      Local Similarity
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les 32; Conserv
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                                                                                                                                                                                                                                                                                Score 22.2;
Pred. No. 10;
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Pred. No. 7.
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CURRENT FILING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: US 60/9
PRIOR FILING DATE: 2004-03-27
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 773
TYPE: DNA
ORGANISM: Artificial Sequence
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; LOCATION: (3)..(767)
US-11-075-891-9
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                                                                                                                                            Sequence 11, Application US/11075891
Publication No. US20060088521A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 773
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Best Local Similarity
APPLICANT: MAHADEVAN, DARUKA
TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
FILE REFERENCE: 263920196
CURRENT APPLICATION NUMBER: US/11/075,891
CURRENT FILING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: US 60/557,258
PRIOR APPLICATION NUMBER: US 60/557,258
PRIOR FILING DATE: 2004-03-27
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: US 60/557,258
PRIOR FILING DATE: 2004-03-27
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CURRENT APPLICATION NUMBER: US/11/075,891
CURRENT FILING DATE: 2005-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: COMPOSITION AND METHOD FILE REFERENCE: 263922US96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MAHADEVAN, DARUKA
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NAME/KEY: CDS
LOCATION: (3).
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OTHER INFORMATION: Synthetic Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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Pred. No. 10;
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Pred. No. 10
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; NAME/KEY: CDS
; LOCATION: (3)..(767)
US-11-075-891-11
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US-11-075-891-13
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                                                                                                                                       Sequence 15, Application US/11075891
Publication No. US20060088521A1
GENERAL INFORMATION:
APPLICANT: MAHADEVAN, DARUKA
TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
FILE REFERENCE: 263922US96
CURRENT APPLICATION NUMBER: US/11/075,891
CURRENT FILING DATE: 2005-03-10
                                                     SEQ ID NO 15
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Publication No. US20060088521A1
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Best Local Similarity
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LENGTH: 773
                                                                        PRIOR APPLICATION NUMBER: US 60/557,258
PRIOR FILING DATE: 2004-03-27
NUMBER OF SEQ ID NOS: 36
SOFTWARR - ------
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TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
FILE REFERENCE: 263920US6
CURRENT APPLICATION NUMBER: US/11/075,891
CURRENT FILING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: US 60/557,258
PRIOR APPLICATION NUMBER: US 60/557,258
PRIOR FILING DATE: 2004-03-27
NUMBER OF SEQ ID NOS: 36
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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TYPE: DNA
ORGANISM: Artificial Sequence
                    TYPE: DNA
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Pred. No. 10;
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Pred. No. 10;
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Sequence 19, Application US/11075891

Publication No. US20060088521A1

GENERAL INFORMATION:
APPLICANT: MAHADEVAN, DARUKA
ITITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
FILE REFERENCE: 263922US96
CURRENT APPLICATION NUMBER: US/11/075,891
CURRENT FILING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: US 60/557,258
PRIOR APPLICATION NUMBER: US 60/557,258
INUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.3
SEQ ID NO 19
LENGTH: 773
; LOCATION: (3)..(767)
US-11-075-891-19
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US-11-075-891-19/c
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; NAME/KEY: CDS
; LOCATION: (3)..(767)
US-11-075-891-17
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US-11-075-891-17/c
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US-11-075-891-15
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TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
FILE REFERENCE: 263922US96
CURRENT APPLICATION NUMBER: US/11/075,891
CURRENT FILING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: US 60/557,258
PRIOR FILING DATE: 2004-03-27
NUMBER OF SEQ ID NOS: 36
SOFTMARE: Patentin version 3.3
SEQ ID NO 17
LENGTH: 773
TYODE. TANN
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Best Local
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                NAME/KEY: CDS
LOCATION: (3)
                                                          FEATURE:
OTHER INFORMATION: Synthetic Peptide
                                                FEATURE:
                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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les 30; Conservative
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Pred. No. 10;
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Pred. No. 10;
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GENERAL INFORMATION:
APPLICANT: MAHADEVAN, DARUKA
ITITLE OF INVENTION: COMPOSITION AND METHOD FOR
FILE REPERENCE: 263922US96
CURRENT APPLICATION NUMBER: US/11/075,891
CURRENT FILING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: US 60/557,258
PRIOR FILING DATE: 2004-03-27
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.3
SEQ ID NO 21
TENGTH. 773
                                                                                                                                                                                                                                                                               APPLICANT: NAKANUTA, NORIHIRO
APPLICANT: NAKANUTA, NORIHIRO
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITILE OF INVENTION: METHODS FOR ANALYZING GENES OF
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT APPLICATION NUMBER: US/11/217,529
PRIOR APPLICATION WHERE: US/10/932,182
PRIOR FILING DATE: 2004-09-02
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
CODETMADE: DETAILS TO THE TOTAL TO TH
                                                                                                                        ; ORGANISM: Saccharomyces pastorianus US-11-217-529-78814
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      Query Match 37.6%;
Best Local Similarity 64.7%;
Matches 33; Conservative
                                                                                                                                                                                                                                          SEQ ID NO 78814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 78814, Application US/11217529
Publication No. US20060099612A1
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RAME/KEY: CDS
NAME/KEY: (3)..(767)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SUNTORY LIMITED APPLICANT: NAKAO, YOSHIHII APPLICANT: NAKAMURA, NORII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                      TYPE: DNA
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